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SEQUENCE LISTING
               (1) GENERAL INFORMATION:
                     (i) APPLICANT: KNUTZON, DEBORAH
                                      MURKERJI, PRADIP
                                      HUANG, YUNG-SHENG
    10
                                      THURMOND, JENNIFER CHAUDHARY, SUNITA
                                      LEONARD, AMANDA
                    (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
    15
                             OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
                  (iii) NUMBER OF SEQUENCES: 40
                   (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LIMBACH AND LIMBACH LLP
    20
                          (B) STREET: 2001 FERRY BUILDING
(C) CITY: SAN FRANCISCO
                          (D) STATE: CA
(E) COUNTRY: USA
    25
                          (F) ZIP: 941Å1
١. ا
                     (v) COMPUTER READABLE FORM:
Ö
                          (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
    30
                          (D) SOFTWARE: Microsoft Word
εi
                   (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
ľŌ
    35
                            (B) (B) FILING DATE:
                          (C) CLASSIFICATION:
(viii) ATTORNEY/AGENT INFORMATION:
                          (A) NAME: WARD, MICHAEL R.
    40
                          (B) REGISTRATION NUMBER: 38,651
                          (C) REFERENCE/DOCKET NUMBER: CGAB-210
                   (ix) TELECOMMUNICATION INFORMATION:
                          (A) TELEP#ONE: (415) 433-4150
    45
                          (B) TELEFAX: (415) 433-8716
                          (C) TELEX: N/A
               (2) INFORMATION FOR SEQ ID NO:1:
    50
                    (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1617 base pairs
                          (B) TYPE: nucleic acid
                          (C) STRANDEDNESS: single
    55
                          (D) TOPOLOGY: linear
                   (ii) MOLECULE TYPE: other nucleic acid
    60
                   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
              CGACACTCCT TCCTTGTTCT CACCCGTCCT AGTCCCCTTC AACCCCCCTC TTTGACAAAG
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		ACAACAAACC	ATGGCTGCTG	CTCCCAGTGT	GAGGACGTTT	ACTCGGGCCG	AGGTTTTGAA	120
	5	TGCCGAGGCT	CTGAATGAGG	GCAAGAAGGA	TGCCGAGGCA	CCCTTCTTGA	TGATCATCGA	180
	J	CAACAAGGTG	TACGATGTCC	GCGAGTTCGT	CCCTGATCAT	CCCGGTGGAA	GTGTGATTCT	240
		CACGCACGTT	GGCAAGGACG	GCACTGACGT	CTTTGACACT	TTTCACCCCG	AGGCTGCTTG	300
	10	GGAGACTCTT	GCCAACTTTT	ACGTTGGTGA	TATTGACGAG	AGCGACCGCG	ATATCAAGAA	360
		TGATGACTTT	GCGGCCGAGG	TCCGCAAGCT	GCGTACCTTG	TTCCAGTCTC	TTGGTTACTA	420
	15	CGATTCTTCC	AAGGCATACT	ACGCCTTCAA	GGTCTCGTTC	AACCTCTGCA	TCTGGGGTTT	480
		GTCGACGGTC	ATTGTGGCCA	AGTGGGGCCA	GACCTCGACC	CTCGCCAACG	TGCTCTCGGC	540
		TGCGCTTTTG	GGTCTGTTCT	GGCAGCAGTG	CGGATGGTTG	GCTCACGACT	TTTTGCATCA	600
	20	CCAGGTCTTC	CAGGACCGTT	TCTGGGGTGA	TCTTTTCGGC	GCCTTCTTGG	GAGGTGTCTG	660
]		CCAGGGCTTC	TCGTCCTCGT	GGTGGAAGGA	CAAGCACAAC	ACTCACCACG	CCGCCCCAA	720
<u>.</u> U.	25	CGTCCACGGC	GAGGATCCCG	ACATTGACAC	CCACCCTCTG	TTGACCTGGA	GTGAGCATGC	780
ñ		GTTGGAGATG	TTCTCGGATG	TCCCAGATGA	GGAGCTGACC	CGCATGTGGT	CGCGTTTCAT	840
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: å	30	CCTCCAGTCC	ATTCTCTTTG	TGCTGCCTAA	CGGTCAGGCC	CACAAGCCCT	CGGGCGCGCG	960
Ų		TGTGCCCATC	TCGTTGGTCG	AGCAGCTGTC	GCTTGCGATG	CACTGGACCT	GGTACCTCGC	1020
1	35	CACCATGTTC	CTGTTCATCA	AGGATCCCGT	CAACATGCTG	GTGTACTTTT	TGGTGTCGCA	1080
		GGCGGTGTGC	GGAAACTTGT	TGGCGATCGT	GTTCTCGCTC	AACCACAACG	GTATGCCTGT	1140
1		GATCTCGAAG	GAGGAGGCGG	TCGATATGGA	TTTCTTCACG	AAGCAGATCA	TCACGGGTCG	1200
	40	TGATGTCCAC	CCGGGTCTAT	TTGCCAACTG	GTTCACGGGT	GGATTGAACT	ATCAGATCGA	1260
		GCACCACTTG	TTCCCTTCGA	TGCCTCGCCA	CAACTTTTCA	AAGATCCAGC	CTGCTGTCGA	1320
	45	GACCCTGTGC	AAAAAGTACA	ATGTCCGATA	CCACACCACC	GGTATGATCG	AGGGAACTGC	1380
		AGAGGTCTTT	AGCCGTCTGA	ACGAGGTCTC	CAAGGCTGCC	TCCAAGATGG	GTAAGGCGCA	1440
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	50	TGTCAAGTCG	AGCGTTTCTG	GAAAGGATCG	TTCAGTGCAG	TATCATCATT	CTCCTTTTAC	1560
		CCCCCGCTCA	TATCTCATTC	ATTTCTCTTA	TTAAACAACT	TGTTCCCCC	TTCACCG	1617
	55	(2) INFORM	ATION FOR S	EQ ID NO:2:				
	60		EQUENCE CHAR (A) LENGTH: (B) TYPE: and (C) STRANDE	457 amino mino acid DNESS: not	acids			

(ii) MOLECULE TYPE: peptide

		(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	D NO	:2:						
	5	Met 1	Ala	Ala	Ala	Pro 5	Ser	Val	Arg	Thr	Phe 10	Thr	Arg	Ala	Glu	Val 15	Leu
		Asn	Ala	Glu	Ala 20	Leu	Asn	Glu	Gly	Lys 25	Lys	Asp	Ala	Glu	Ala 30	Pro	Phe
	10	Leu	Met	Ile 35	Ile	Asp	Asn	Lys	Val 40	Туг	Asp	Val	Arg	Glu 45	Phe	Val	Pro
		Asp	His 50	Pro	Gly	Gly	Ser	Val 55	Ile	Leu	Thr	His	Val 60	Gly	Lys	Asp	Gly
	15	Thr 65	Asp	Val	Phe	Asp	Thr 70	Phe	His	Pro	Glu	Ala 75	Ala	Trp	Glu	Thr	Leu 80
	20	Ala	Asn	Phe	Tyr	Val 85	Gly	Asp	Ile	Asp	Glu 90	Ser	Asp	Arg	Asp	Ile 95	Lys
:=		Asn	Asp	Asp	Phe 100	Ala	Ala	Glu	Val	Arg 105	Lys	Leu	Arg	Thr	Leu 110	Phe	Gln
e e	25	Ser	Leu	Gly 115	Tyr	Tyr	Asp	Ser	Ser 120	Lys	Ala	Tyr	Tyr	Ala 125	Phe	Lys	Val
		Ser	Phe 130	Asn	Leu	Cys	Ile	Trp 135	Gly	Leu	Ser	Thr	Val 140	Ile	Val	Ala	Lys -
	30	Trp 145	Gly	Gln	Thr	Ser	Thr 150	Leu	Ala	Asn	Val	Leu 155	Ser	Ala	Ala	Leu	Leu 160
	35	Gly	Leu	Phe	Trp	Gln 165	Gln	Cys	Gly	Trp	Leu 170	Ala	His	Asp	Phe	Leu 175	His
ΪŌ		His	Gln	Val	Phe 180	Gln	Asp	Arg	Phe	Trp 185	Gly	Asp	Leu	Phe	Gly 190	Ala	Phe
	40	Leu	Gly	Gly 195	Val	Cys	Gln	Gly	Phe 200	Ser	Ser	Ser	Trp	Trp 205	Lys	Asp	Lys
Transf		His	Asn 210	Thr	His	His	Ala	Ala 215	Pro	Asn	Val	His	Gly 220	Glu	Asp	Pro	Asp
	45	Ile 225	Asp	Thr	His	Pro	Leu 230	Leu	Thr	Trp	Ser	Glu 235	His	Ala	Leu	Glu	Met 240
	50	Phe	Ser	Asp	Val	Pro 245	Asp	Glu	Glu	Leu	Thr 250	Arg	Met	Trp	Ser	Arg 255	Phe
		Met	Val	Leu	Asn 260	Gln	Thr	Trp	Phe	Tyr 265	Phe	Pro	Ile	Leu	Ser 270	Phe	Ala
	55	Arg	Leu	Ser 275	Trp	Cys	Leu	Gln	Ser 280	Ile	Leu	Phe	Val	Leu 285	Pro	Asn	Gly
		Gln	Ala 290	His	Lys	Pro	Ser	Gly 295	Ala	Arg	Val	Pro	Ile 300	Ser	Leu	Val	Glu
	60	Gln 305	Leu	Ser	Leu	Ala	Met 310	His	Trp	Thr	Trp	Tyr 315	Leu	Ala	Thr	Met	Phe 320
77	-6 5_	Leu	Phe	Ile	Lys	Asp 325	Pro	Val	Asn	Met	Leu 330	Val	Tyr	Phe	Leu	Val 335	Ser
		Gln	Ala	Val	Cys	Gly	Asn	Leu	Leu	Ala	Ile	Val	Phe	Ser	Leu	Asn	His

					340					345					350			
	E	Asn	Gly	Met 355	Pro	Val	Ile	Ser	Lys 360	Glu	Glu	Ala	Val	Asp 365	Met	Asp	Phe	
	5	Phe	Thr 370	Lys	Gln	Ile	Ile	Thr 375	Gly	Arg	Asp	Val	His 380	Pro	Gly	Leu	Phe	
	10	Ala 385	Asn	Trp	Phe	Thr	Gly 390	Gly	Leu	Asn	Tyr	Gln 395	Ile	Glu	His	His	Leu 400	
		Phe	Pro	Ser	Met	Pro 405	Arg	His	Asn	Phe	Ser 410	Lys	Ile	Gln	Pro	Ala 415	Val	
	15	Glu	Thr	Leu	Cys 420	Lys	Lys	Tyr	Asn	Val 425	Arg	Tyr	His	Thr	Thr 430	Gly	Met	
	20	Ile	Glu	Gly 435	Thr	Ala	Glu	Val	Phe 440	Ser	Arg	Leu	Asn	Glu 445	Val	Ser	Lys	
-		Ala	Ala 450	Ser	Lys	Met	Gly	Lys 455	Ala	Gln								
7	25	(2) INFO	RMAT	ION I	FOR S	SEQ :	ID N	3:3:										
es and Gree heal	23	(i)	(A) LEI	E CHANGTH:	148	88 ba	ase p		5								
4 4 4 5 5 cm	30		(C) STI	RANDI POLO	EDNE:	ss: :	sing.	le									
1		(ii)	MOL	ECULI	E TYI	PE: 1	DNA	(gen	omic)								
	35																	
		(xi)	SEQ	UENC	E DES	SCRI	PTIO	N: S1	EQ II	D NO	:3:							
1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.	40	GTCCCCTG	TC G	CTGT	CGGC	A CA	cccc	ATCC	TCC	CTCG	CTC	CCTC	TGCG	rt t	GTCC	TTGG	С	60
_		CCACCGTC	TC T	CCTC	CACC	C TC	CGAG	ACGA	CTG	CAAC'	TGT .	AATC	AGGA	AC C	GACA	AATA	С	120
		ACGATTTC	TT T	TTAC'	TCAG	CAC	CAAC	rcaa	AAT	CCTC	AAC	CGCA	ACCC'	TT T	TTCA	GGAT	G	180
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	50	ATCCGAGA	GT G	CATC	CCTG	C CC	ACTG	CTTT	GAG	CGCT	CCG	GTCT	CCGT	GG T	CTCT	GCCA	С	360
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	*	TTTGAGAA	TC C	CTTG	ATCC	G CT	TTTA	GGCC	TGG	CCTG	TTT	ACTG	GATC	AT G	CAGG	GTAT	Т	480
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	60	TCCTGGAG	AA T	CTCG	CACT	C GA	AGCA	CCAC	AAG	GCCA	CTG	GCCA	TATG	AC C	AAGG	ACCA	G	660
		GTCTTTGT	GC C	CAAG	ACCC	G CT	CCCA	GGTT	GGC	TTGC	CTC	CCAA	GGAG	AA C	GCTG	CTGC	T	720
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	-65	TTCTGGAT	GG T	GATC	CAGT	т ст	TGTT	CGGA	TGG	CCCG	CGT	ACCT	GATT	AT G	AACG	CCTC	T	840

		GGCCAAGA	CT A	.CGGC	CGCT	G GA	CCTC	GCAC	TTC	CACA	CGT	ACTC	GCCC	AT C	TTTG	AGCC	c	900
		CGCAACTT	TT T	CGAC	ATTA	TA	TCTC	GGAC	CTC	GGTG	TGT	TGGC	TGCC	CT C	GGTG	CCCT	G	960
	5	ATCTATGO	CT C	CATG	CAGT	r GT	CGCT	CTTG	ACC	GTCA	CCA	AGTA	CTAT	T TA	GTCC	CCTA	c	1020
		CTCTTTGT	CA A	CTTT	TGGT	r GG	TCCT	GATC	ACC	TTCT	TGC	AGCA	CACC	GA T	CCCA	AGCT	G	1086
	10	CCCCATTA	CC G	CGAG	GGTG	CT	GGAA	TTTC	CAG	CGTG	GAG	стст	TTGC	AC C	GTTG.	ACCG	С	1140
		TCGTTTGG	CA A	GTTC	TTGG	A CC	ATAT	GTTC	CAC	GGCA	TTG	TCCA	CACC	CA T	GTGG	CCCA	T	1200
		CACTTGTT	CT C	GCAA	ATGC	GT	TCTA	CCAT	GCT	GAGG.	AAG	CTAC	CTAT	CA T	CTCA	AGAA	A	1260
	15	CTGCTGGG	AG A	GTAC	TATGI	GT.	ACGA	CCCA	TCC	CCGA'	TCG	TCGT	TGCG	GT C	TGGA	GGTC	G	1320
		TTCCGTGA	GT G	CCGA	TTCGI	GG.	AGGA'	TCAG	GGA	GACG'	TGG	TCTT	TTTC.	AA G	AAGT	AAAA	A	1380
	20	AAAAGACA	AT G	GACC.	ACACA	A CA	ACCT'	TGTC	TCT	ACAG	ACC '	TACG	TATC	AT G	TAGC	CATA	С	1440
		CACTTCAT	AA A	AGAA	CATGA	GC'	TCTA	GAGG	CGT	GTCA'	TTC	GCGC	CTCC					1488
	2.5	(2) INFO	RMAT	ION	FOR S	SEQ	ID N	0:4:										
J	25	(i)	SEQ (A	UENCI	E CHA	RAC'	TERI: 9 am:	STIC:	S: acid:	s								
1 1 1 1 1 1 1 1			(B (C) TY:	PE: a RANDE	min DNE	o ac: SS: 1	id not :										
	30		(D) TO:	POLOG	SY:	line	ar										
i.		(ii)	MOL	ECULI	E TYF	PE: 1	p ept :	ide			٠							
E:	25																	
[] [0	35	(xi)	SEQ	UENCI	E DES	CRI	PTIO	N: SI	EQ II	D NO	:4:							
		Met	Ala	Pro	Pro	Asn	Thr	Ile	Asp	Ala	Gly	Leu	Thr	Gln	Arg	His	Ile	
ŧ.:∎	40	1				5					10					15		
ij		Ser	Thr	Ser	Ala 20	Pro	Asn	Ser	Ala	Lys 25	Pro	Ala	Phe	Glu	Arg 30	Asn	Tyr	
	45	Gln	Leu	Pro	Glu	Phe	Thr	Ile	Lys	Glu	Ile	Arg	Glu	Cys	Ile	Pro	Ala	
		Hie	Cur	35 Bho	C1	D	0		40					45				
		nis	50 50	rne	Glu	Arg	ser	55 55	Leu	Arg	Gly	Leu	Cys 60	His	Val	Ala	Ile	
	50	Asp 65	Leu	Thr	Trp	Ala	Ser	Leu	Leu	Phe	Leu	Ala	Ala	Thr	Gln	Ile	Asp	
			Phe	Gl II	Acn	Pro	70	T1.	N		_	75	_				80	
	55	2,0	1110	Giu	Asn	85	rea	116	Arg	Tyr	90	Ala	Trp	Pro	Val	Tyr 95	Trp	
		Ile	Met	Gln	Gly 100	Ile	Val	Cys	Thr	Gly 105	Val	Trp	Val	Leu		His	Glu	
		Cys	Glv	His	Gln	Ser	Phe	Ser	Thr		1	mb ==	T	>	110		,	
	60	-	-	115					120	261	nys	IIIE	red	125	ASN	Tnr	val	
		Gly	Trp 130	Ile	Leu	His	Ser	Met 135	Leu	Leu	Val	Pro	Tyr 140	His	Ser	Trp	Arg	
77	65	Ile	Ser	His	Ser	Lys	His		Lvs	Ala	Thr	Glv		Met	ምኮ ፦	Luc	λοπ	
		145					150					155		17E C	THE	nλ2	160	

			Gin	Val	Phe	Val	Pro 165	Lys	Thr	Arg	Ser	Gln 170	Val	Gly	Leu	Pro	Pro 175	Lys
	5		Glu	Asn	Ala	Ala 180	Ala	Ala	Val	Gln	Glu 185	Glu	Asp	Met	Ser	Val 190	His	Leu
	10		Asp	Glu	Glu 195	Ala	Pro	Ile	Val	Thr 200	Leu	Phe	Trp	Met	Val 205	Ile	Gln	Phe
	10		Leu	Phe 210	Gly	Trp	Pro	Ala	Tyr 215	Leu	Ile	Met	Asn	Ala 220	Ser	Gly	Gln	Asp
	15		Tyr 225	Gly	Arg	Trp	Thr	Ser 230	His	Phe	His	Thr	Tyr 235	Ser	Pro	Ile	Phe	Glu 240
			Pro	Arg	Asn	Phe	Phe 245	Asp	Ile	Ile	Ile	Ser 250	Asp	Leu	Gly	Val	Leu 255	Ala
	20		Ala	Leu	Gly	Ala 260	Leu	Ile	Tyr	Ala	Ser 265	Met	Gln	Leu	Ser	Leu 270	Leu	Thr
11 11.	25		Val	Thr	Lys 275	Tyr	Tyr	Ile	Val	Pro 280	Tyr	Leu	Phe	Val	Asn 285	Phe	Trp	Leu
			Val	Leu 290	Ile	Thr	Phe	Leu	Gln 295	His	Thr	Asp	Pro	Lys 300	Leu	Pro	His	Tyr
4 7 4	30		Arg 305	Glu	Gly	Ala	Trp	Asn 310	Phe	Gln	Arg	Gly	Ala 315	Leu	Cys	Thr	Val	Asp 320
j.			Arg	Ser	Phe	Gly	Lys 325	Phe	Leu	Asp	His	Met 330	Phe	His	Gly	Ile	Val 335	His
F1 4.74 F	35		Thr	His	Val	Ala 340	His	His	Leu	Phe	Ser 345	Gln	Met	Pro	Phe	Tyr 350	His	Ala
LI G.I I G.I G.B C.I	40		Glu	Glu	Ala 355	Thr	Tyr	His	Leu	Lys 360	Lys	Leu	Leu	Gly	Glu 365	туг	Tyr	Val
11.4			Туr	Asp 370	Pro	Ser	Pro	Ile	Val 375	Val	Ala	Val	Trp	Arg 380	Ser	Phe	Arg	Glu
	45		Cys 385	Arg	Phe	Val	Glu	Asp 390	Gln	Gly	Asp	Val	Val 395	Phe	Phe	Lys	Lys	
		(2)	INFO	RMAT	ON I	FOR S	SEQ :	ID NO	0:5:									
	50		(i)	(A) (B) (C)	LEN TYI	NGTH PE: 8	ARAC: 35! amino EDNE: GY:	5 am: 5 ac: SS: 1	ino a id	acid								
	55		(ii)	MOLI	ECULI	E TY	PE:	pept:	ide									
	60		(xi)	SEQ	JENCI	E DES	SCRI	PTIO	N: S	EQ I	D NO	:5:						
			Glu 1	Val	Arg	Lys	Leu 5	Arg	Thr	Leu	Phe	Gln 10	Ser	Leu	Gly	Tyr	Tyr 15	Asp
=	-65		Ser	Ser	Lys	Ala 20	Tyr	Tyr	Ala	Phe	Lys 25	Val	Ser	Phe	Asn	Leu 30	Cys	Ile

			Trp	Gly	Leu 35	Ser	Thr	Val	Ile	Val	Ala	Lys	Trp	Gly	Gln 45	Thr	Ser	Thr
	5		Leu	Ala 50	Asn	Val	Leu	Ser	Ala 55	Ala	Leu	Leu	Gly	Leu 60	Phe	Trp	Gln	Gln
	10		Cys 65	Gly	Trp	Leu	Ala	His 70	Asp	Phe	Leu	His	His 75	Gln	Val	Phe	Gln	Asp 80
			Arg	Phe	Trp	Gly	Asp 85	Leu	Phe	Gly	Ala	Phe 90	Leu	Gly	Gly	Val	Cys 95	Gln
	15		Gly	Phe	Ser	Ser 100	Ser	Trp	Trp	Lys	Asp 105	Lys	His	Asn	Thr	His 110	His	Ala
			Ala	Pro	Asn 115	Val	His	Gly	Glu	Asp 120	Pro	Asp	Ile	Asp	Thr 125	His	Pro	Leu
	20		Leu	Thr 130	Trp	Ser	Glu	His	Ala 135	Leu	Glu	Met	Phe	Ser 140	Asp	Val	Pro	Asp
	25		Glu 145	Glu	Leu	Thr	Arg	Met 150	Trp	Ser	Arg	Phe	Met 155	Val	Leu	Asn	Gln	Thr 160
Arm and than that					Tyr		163					170					175	
F. 4.	30				Ile	100					185					190		
	25				Arg 195					200					205			
	35		His	Trp 210	Thr	Trp	Tyr	Leu	Ala 215	Thr	Met	Phe	Leu	Phe 220	Ile	Lys	Asp	Pro
	40		223		Met			230					235					240
.3					Ala		245					250					255	
	45				Glu	200					265					270	-	_
	50				Arg 275					280					285			
	50			250	Asn				295					300				
	55				Phe			310					315					320
					Val		323					330					335	
	60		Val	Phe	Ser	Arg 340	Leu	Asn	Glu	Val	Ser 345	Lys	Ala	Ala	Ser	Lys 350	Met	Gly
	65		Lys		355													
79	.65	(2)	INFOR	ITAM	ON F	OR S	EQ I	D NO	:6:									

PCT/US98/07126 WO 98/46763

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids
(B) TYPE: amino acid

	5				STR	ANDE	DNES	SS: n	ot r	elev	ant							
			(ii)	MOLE	CULE	TYP	E: p	epti	.de									
	10																	
			(xi)	SEQU	JENCE	DES	CRIE	MOITS	: SE	Q IC	NO:	6:						
	15		Val 1	Thr	Leu	Tyr	Thr 5	Leu	Ala	Phe	Val	Ala 10	Ala	Asn	Ser	Leu	Gly 15	Val
			Leu	Tyr	Gly	Val 20	Leu	Ala	Cys	Pro	Ser 25	Val	Xaa	Pro	His	Gln 30	Ile	Ala
	20		Ala	Gly	Leu 35	Leu	Gly	Leu	Leu	Trp 40	Ile	Gln	Ser	Ala	Tyr 45	Ile	Gly	Xaa
	25		Asp	Ser 50	Gly	His	Tyr	Val	Ile 55	Met	Ser	Asn	Lys	Ser 60	Asn	Asn	Xaa	Phe
اليما الإسادة اليما الإسادة اليما اليما اليما اليما اليما			Ala 65	Gln	Leu	Leu	Ser	Gly 70	Asn	Cys	Leu	Thr	Gly 75	Ile	Ile	Ala	Trp	Trp 80
1775 H	30		Lys	Trp	Thr	His	Asn 85	Ala	His	His	Leu	Ala 90	Cys	Asn	Ser	Leu	Asp 95	Tyr
14 11 11			Gly	Pro	Asn	Leu 100	Gln	His	Ile	Pro								
: -2 (:0	35	(2)	INFO	RMAT	ton i	FOR S	SEQ :	ID NO	0:7:									
The first time that the first time	40		(i)	(A) (B) (C)	LEI TYI STI	NGTH: PE: & RANDE	25: mine EDNE:	renis 2 am: 5 ac: SS: r	ino a id not i	acids								
			(ii)	MOL	ECUL	E TY	PE: 1	pept:	ide									
	45																	
			(xi)	SEQ	JENCI	E DES	SCRI	PTIO	N: S	EQ II	ON C	:7:						
	50		Gly 1	Val	Leu	Tyr	Gly 5	Val	Leu	Ala	Cys	Thr 10	Ser	Val	Phe	Ala	His 15	Gln
	55		Ile	Ala	Ala	Ala 20	Leu	Leu	Gly	Leu	Leu 25	Trp	Ile	Gln	Ser	Ala 30	Tyr	Ile
			Gly	His	Asp 35	Ser	Gly	His	Tyr	Val 40	Ile	Met	Ser	Asn	Lys 45	Ser	Tyr	Asn
	60		Arg	Phe 50	Ala	Gln	Leu	Leu	Ser 55	Gly	Asn	Cys	Leu	Thr 60	Gly	Ile	Ser	Ile
			Ala 65	Trp	Trp	Lys	Trp	Thr 70	His	Asn	Ala	His	His 75	Leu	Ala	Cys	Asn	Ser 80
7	65		Leu	Asp	Туr	Asp	Pro 85	Asp	Leu	Gln	His	Ile 90	Pro	Val	Phe	Ala	Val 95	Ser
											100							

		Thr	Lys	Phe	Phe 100	Ser	Ser	Leu	Thr	Ser 105	Arg	Phe	Туr	Asp	Arg 110	Lys	Leu
	5	Thr	Phe	Gly 115	Pro	Val	Ala	Arg	Phe 120	Leu	Val	Ser	Туr	Gln 125	His	Phe	Thr
	10	Tyr	Tyr 130	Pro	Val	Asn	Cys	Phe 135	Gly	Arg	Ile	Asn	Leu 140	Phe	Ile	Gln	Thr
		Phe 145	Leu	Leu	Leu	Phe	Ser 150	Lys	Arg	Glu	Val	Pro 155	Asp	Arg	Ala	Leu	Asn 160
	15	Phe	Ala	Gly	Ile	Leu 165	Val	Phe	Trp	Thr	Trp 170	Phe	Pro	Leu	Leu	Val 175	Ser
	•	Cys	Leu	Pro	Asn 180	Trp	Pro	Glu	Arg	Phe 185	Phe	Phe	Val	Phe	Thr 190	Ser	Phe
	20	Thr	Val	Thr 195	Ala	Leu	Gln	His	11e 200	Gln	Phe	Thr	Leu	Asn 205	His	Phe	Ala
	25	Ala	Asp 210	Val	Tyr	Val	Gly	Pro 215	Pro	Thr	Gly	Ser	Asp 220	Trp	Phe	Glu	Lys
		Gln 225	Ala	Ala	Gly	Thr	Ile 230	Asp	Ile	Ser	Cys	Arg 235	Ser	Tyr	Met	Asp	Trp 240
الما إما سية المستقل الما الما الما الما الما الما الما ال	30	Phe	Phe	Gly	Gly	Leu 245	Gln	Phe	Gln	Leu	Glu 250	His	His				
1. U		(2) INFO	RMAT	ION I	FOR S	SEQ :	ID NO	0:8:									
THE PART OF STREET	35	<u>,</u> (i)	(A) (B) (C)	JENCE) LEN) TYI) STI) TOI	NGTH: PE: 6 RANDE	: 12! amino EDNE:	ami aci	ino a id not 1	cids								
R. Han Bang	40	(ii)	MOLI	ECULE	E TY	PE: p	pepti	ide									
	45	(xi)	SEQ	JENCE	E DES	SCRII	PTION	1: SE	Q II	NO:	8:						
		Gly 1	Xaa	Xaa	Asn	Phe 5	Ala	Gly	Ile	Leu	Val 10	Phe	Trp	Thr	Trp	Phe 15	Pro
	50	Leu	Leu	Val	Ser 20	Cys	Leu	Pro	Asn	Trp 25	Pro	Glu	Arg	Phe	Xaa 30	Phe	Val
		Phe	Thr	Gly	Phe	Thr	Val	Thr	Δla	ī.e.i	C1-	Hie	Tla	Gln	Dha	m b	Lou
	55			35					40	Deu	GIII		116	45	rne	Inr	Leu
	55			35 Phe					40					45			
	5560	Asn	His 50	33	Ala	Ala	Asp	Val 55	40 Tyr	Val	Gly	Pro	Pro 60	45 Thr	Gly	Ser	Asp
		Asn	His 50 Phe	Phe Glu	Ala Lys	Ala Gln	Asp Ala 70	Val 55 Ala	40 Tyr Gly	Val Thr	Gly Ile	Pro Asp 75	Pro 60	45 Thr Ser	Gly Cys	Ser Arg	Asp Ser 80

			Gly	Gln	Arg 115	Gly	Phe	Gln	Arg	Lys 120	Xaa	Asn	Leu	Ser	Xaa 125			
	5	(2)	INFOR	ITAMS	ON E	FOR S	EQ I	D NC):9:									
	10		(i)	(A) (B) (C)	LEN TYP STF	IGTH: PE: & RANDE	131 minc DNES	TERIS ami aci SS: n	no a d ot r	cids								
			(ii)	MOLE	CULE	TYE	E: p	epti	.de									
	15																	
			(xi)	SEQU	ENCE	DES	CRIE	OITS	: SE	Q II	NO:	9:						
	20		Pro 1	Ala	Thr	Glu	Val 5	Gly	Gly	Leu	Ala	Trp 10	Met	Ile	Thr	Phe	Tyr 15	Val
	25		Arg	Phe	Phe	Leu 20	Thr	Tyr	Val	Pro	Leu 25	Leu	Gly	Leu	Lys	Ala 30	Phe	Leu
			Gly	Leu	Phe 35	Phe	Ile	Val	Arg	Phe 40	Leu	Glu	Ser	Asn	Trp 45	Phe	Val	Trp
21 002	30		Val	Thr 50	Gln	Met	Asn	His	Ile 55	Pro	Met	His	Ile	Asp 60	His	Asp	Arg	Asn
IJ.			Met 65	Asp	Trp	Val	Ser	Thr 70	Gln	Leu	Gln	Ala	Thr 75	Cys	Asn	Val	His	Lys 80
	35		Ser	Ala	Phe	Asn	Asp 85	Trp	Phe	Ser	Gly	His 90	Leu	Asn	Phe	Gln	Ile 95	Glu
	40		His	His	Leu	Phe 100	Pro	Thr	Met	Pro	Arg 105	His	Asn	Tyr	His	Xaa 110	Val	Ala
			Pro	Leu	Val 115	Gln	Ser	Leu	Cys	Ala 120	Lys	His	Gly	Ile	Glu 125	Tyr	Gln	Ser
	45		Lys	Pro 130	Leu													
		(2)	INFOR	(TAMS	ON I	FOR S	SEQ :	ID NO	0:10:	:								
	50		(i)	(A) (B) (C)	LEN TYI STI	NGTH: PE: 8 RANDI	: 87 mino EDNE:	reris amin aci ss: n linea	no ad id not i	cids	vant							
	55		(ii)	MOLE	ECULI	E TYI	PE: 1	pept:	ide									
	60		(xi)	SEQU	JENCI	E DES	SCRI	PTIO	N: SI	EQ II	ои о	:10:						
			Cys 1	Ser	Pro	Lys	Ser 5	Ser	Pro	Thr	Arg	Asn 10	Met	Thr	Pro	Ser	Pro 15	Phe
7	-6 5		Ile	Asp	Trp	Leu 20	Trp	Gly	Gly	Leu	Asn 25	Tyr	Gln	Ile	Glu	His 30	His	Leu

			Phe	Pro	Thr 35	Met	Pro	Arg	Cys	Asn 40	Leu	Asn	Arg	Cys	Met 45	Lys	Tyr	Val
	5		Lys	Glu 50	Trp	Cys	Ala	Glu	Asn 55	Asn	Leu	Pro	Tyr	Leu 60	Val	Asp	Asp	Tyr
	10		Phe 65	Val	Gly	Tyr	Asn	Leu 70	Asn	Leu	Gln	Gln	Leu 75	Lys	Asn	Met	Ala	Glu 80
	10		Leu	Val	Gln	Ala	Lys 85	Ala	Ala									
	15	(2)	INFO	RMAT	ION	FOR :	SEQ	ID N	0:11	:								
			(i)	(A (B	UENC:	NGTH	: 14: amin	am: ac:	ino a id	acid:								
	20			(C) STI	POLO	EDNE:	SS: 1	not :	rele	vant							
			(ii)	MOL	ECULI	E TYI	PE: 1	pept:	ide									
And Mine Hall	25																	
n n			(xi)	SEQ	JENCI	E DES	CRI	PTIO	N: SI	EQ II	001	:11:						
Vi Und dies	30		Arg 1	His	Glu	Ala	Ala 5	Arg	Gly	Gly	Thr	Arg 10	Leu	Ala	Tyr	Met	Leu 15	Val
1			Cys	Met	Gln	Trp 20	Thr	Asp	Leu	Leu	Trp 25	Ala	Ala	Ser	Phe	Tyr 30	Ser	Arg
ili ilili ilili	35		Phe	Phe	Leu 35	Ser	Tyr	Ser	Pro	Phe 40	Tyr	Gly	Ala	Thr	Gly 45	Thr	Leu	Leu
וניים וניים וניים וניים וניים וניים	40		Leu	Phe 50	Val	Ala	Val	Arg	Val 55	Leu	Glu	Ser	His	Trp 60	Phe	Val	Trp	Ile
II.JI			Thr 65	Gln	Met	Asn	His	Ile 70	Pro	Lys	Glu	Ile	Gly 75	His	Glu	Lys	His	Arg 80
	45		Asp	Trp	Ala	Ser	Ser 85	Gln	Leu	Ala	Ala	Thr 90	Cys	Asn	Val	Glu	Pro 95	Ser
			Leu	Phe	Ile	Asp 100	Trp		Ser				Asn		Gln		Glu	His
	50		His	Leu	Phe 115	Pro	Thr	Met	Thr	Arg 120	His	Asn	туг				Ala	Pro
	55		Leu	Val 130	Lys	Ala	Phe	Cys	Ala 135	Lys	His	Gly	Leu	His 140	Туг	Glu	Val	
	55	(2)	INFOR	I TAMS	ON E	OR S	EQ 1	D NC	:12:									
	60	÷	(i)	(A) (B) (C)	JENCE LEN TYE STE TOE	GTH: E: n ANDE	35 ucle DNES	base ic a SS: s	pai cid ingl	rs								
,	-65		(ii)	MOLE	CULE	TYF	E: c	ther	nuc	leic	aci	.d						

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that the family that that

		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
	5	CCAAGCTTCT GCAGGAGCTC TTTTTTTTT TTTTT 3	5
		(2) INFORMATION FOR SEQ ID NO:13:	
	10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	15	(ii) MOLECULE TYPE: other nucleic acid	
	20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
1 ⁶ 11 ¹ 1 ¹ 1		CUACUACUAC UAGGAGTCCT CTACGGTGTT TTG	33
	25	(2) INFORMATION FOR SEQ ID NO:14:	
In And then will thin In	30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
4	50		
		(ii) MOLECULE TYPE: other nucleic acid	
j	35		
Und Und Will Und Wild Und		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
144	40	CAUCAUCAUC AUATGATGCT CAAGCTGAAA CTG	33
14.13 13.13	10	(2) INFORMATION FOR SEQ ID NO:15:	
	45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	50	(ii) MOLECULE TYPE: other nucleic acid	
	55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
		TACCAACTCG AGAAAATGGC TGCTGCTCCC AGTGTGAGG	39
	60	(2) INFORMATION FOR SEQ ID NO:16:	•
	60	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
***	65	(ii) MOLECULE TYPE: other nucleic acid	

	5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
		AACTGATCTA GATTACTGCG CCTTACCCAT CTTGGAGGC	39
	10	(2) INFORMATION FOR SEQ ID NO:17:	
	15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
		(ii) MOLECULE TYPE: other nucleic acid	
	20		
:5		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
3	25	TACCAACTCG AGAAAATGGC ACCTCCCAAC ACTATCGAT	39
j		(2) INFORMATION FOR SEQ ID NO:18:	
tim to the steer and time test	30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	35	(ii) MOLECULE TYPE: other nucleic acid	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
H., II V., I	40	AACTGATCTA GATTACTTCT TGAAAAAGAC CACGTCTCC	. 39
		(2) INFORMATION FOR SEQ ID NO:19:	
	45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 746 nucleic acids (B) TYPE: nucleic acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: linear 	
	50	(ii) MOLECULE TYPE: nucleic acid	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
	55	CGTATGTCAC TCCATTCCAA ACTCGTTCAT GGTATCATAA ATATCAACAC ATTTACGCTC CACTCCTCTA TGGTATTAC ACACTCAAAT ATCGTACTCA AGATTGGGAA GCTTTTGTAA AGGATGGTAA AAATGGTGCA ATTCGTGTTA GTGTCGCCAC AAATTTCGAT AAGGCCGCTT ACGTCATTGG TAAATTGTCT TTTGTTTTCT TCCGTTTCAT CCTTCCACTC CGTTATCATA GCTTTACAGA TTTAATTTGT TATTTCCTCA TTGCTGAATT CGTCTTTGGT TGGTATCTCA	60 120 180 240 300
	60	GACCAGATGA ACCATTAGT CATGTCGCTG AAGATCTCAA ATTCTTTGCT ACCCCTGAAA GACCAGATGA ACCATCTCAA ATCAATGAAG ATTGGGCAAT CCTTCAACTT AAAACTACTC AAGATTATGG TCATGGTTCA CTCCTTTGTA CCTTTTTTAG TGGTTCTTTA AATCATCAAG TTGTTCATCA TTTATTCCCA TCAATTGCTC AAGATTTCTA CCCACAACTT GTTACCAATTG TAAAAGAAGT TTGTAAAGAA CATAACATTA CTTACCACAT TAAACGAAGT	360 420 480 540 600
•	65	CTATTATGTC ACACATTAAT TACCTTTACA AAATGGGTAA TGATCCAGAT TATGTTAAAA AACCATTAGC CTCAAAAGAT GATTAAATGA AATAACTTAA AAACCAATTA TTTACTTTTG	660 720

ACAAACAGTA ATATTAATAA ATACAA 746

(2) INFORMATION FOR SEO ID NO: 20:

```
5
                  (i) SEQUENCE CHARACTERISTICS:
                       (A) LENGTH: 227 amino acids
                       (B) TYPE: amino acid
                       (C) STRANDEDNESS: not relevant
   10
                       (D) TOPOLOGY: linear
                 (ii) MOLECULE TYPE: peptide
                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
   15
            Tyr Val Thr Pro Phe Gln Thr Arg Ser Trp Tyr His Lys Tyr Gln
                                                                      15
            His Ile Tyr Ala Pro Leu Leu Tyr Gly Ile Tyr Thr Leu Lys Tyr
                              20
                                                  25
                                                                      30
   20
            Arg Thr Gln Asp Trp Glu Ala Phe Val Lys Asp Gly Lys Asn Gly
                                                  40
                                                                      45
            Ala Ile Arg Val Ser Val Ala Thr Asn Phe Asp Lys Ala Ala Tyr
                              50
                                                  55
                                                                       60
            Val Ile Gly Lys Leu Ser Phe Val Phe Phe Arg Phe Ile Leu Pro
   25
                              65
                                                  70
            Leu Arg Tyr His Ser Phe Thr Asp Leu Ile Cys Tyr Phe Leu Ile
ľΝ
                              80
                                                  85
            Ala Glu Phe Val Phe Gly Trp Tyr Leu Thr Ile Asn Phe Gln Val
                              95
                                                 100
   30
            Ser His Val Ala Glu Asp Leu Lys Phe Phe Ala Thr Pro Glu Arg
                             110
                                                 115
IJ
            Pro Asp Glu Pro Ser Gln Ile Asn Glu Asp Trp Ala Ile Leu Gln
                             125
                                                 130
            Leu Lys Thr Thr Gln Asp Tyr Gly His Gly Ser Leu Leu Cys Thr
                             140
                                                 145
            Phe Phe Ser Gly Ser Leu Asn His Gln Val Val His His Leu Phe
155
                                                 160
                                                                      165
            Pro Ser Ile Ala Gln Asp Phe Tyr Pro Gln Leu Val Pro Ile Val
170
                                                 175
:,]
   40
            Lys Glu Val Cys Lys Glu His Asn Ile Thr Tyr His Ile Lys Pro
                             185
                                                 190
                                                                      195
            Asn Phe Thr Glu Ala Ile Met Ser His Ile Asn Tyr Leu Tyr Lys
                             200
                                                 205
            Met Gly Asn Asp Pro Asp Tyr Val Lys Lys Pro Leu Ala Ser Lys
   45
                             215
                                                 220
            Asp Asp ***
             (2) INFORMATION FOR SEQ ID NO 21:
   50
                  (i) SEQUENCE CHARACTERISTICS:
                       (A) LENGTH: 494 nucleic acids
                       (B) TYPE: nucleic acid
                       (C) STRANDEDNESS: not relevant
   55
                       (D) TOPOLOGY: linear
                 (ii) MOLECULE TYPE: nucleic acid
                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
   60
            TTTTGGAAGG NTCCAAGTTN ACCACGGANT NGGCAAGTTN ACGGGGCGGA AANCGGTTTT
            CCCCCAAGC CTTTTGTCGA CTGGTTCTGT GGTGGCTTCC AGTACCAAGT CGACCACCAC
                                                                                  120
            TTATTCCCCA GCCTGCCCCG ACACAATCTG GCCAAGACAC ACGCACTGGT CGAATCGTTC
                                                                                  180
  -65
            TGCAAGGAGT GGGGTGTCCA GTACCACGAA GCCGACCTCG TGGACGGGAC CATGGAAGTC
                                                                                  240
            TTGCACCATT TGGGCAGCGT GGCCGGCGAA TTCGTCGTGG ATTTTGTACG CGACGGACCC
                                                                                  300
```

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GCCATGTAAT CGTCGTTCGT GACGATGCAA GGGTTCACGC ACATCTACAC ACACTCACTC
              ACACAACTAG TGTAACTCGT ATAGAATTCG GTGTCGACCT GGACCTTGTT TGACTGGTTG
                                                                                      420
              GGGATAGGGT AGGTAGGCGG ACGCGTGGGT CGNCCCCGGG AATTCTGTGA CCGGTACCTG
                                                                                     480
              GCCCGCGTNA AAGT
                                                                                      494
      5
              (2) INFORMATION FOR SEQ ID NO:22:
     10
                   (i) SEQUENCE CHARACTERISTICS:
                         (A) LENGTH: 87 amino acids
                         (B) TYPE: amino acid
                         (C) STRANDEDNESS: not relevant
                         (D) TOPOLOGY: linear
     15
                  (ii) MOLECULE TYPE: peptide
              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
     20
              Phe Trp Lys Xxx Pro Ser Xxx Pro Arg Xxx Xxx Gln Val Xxx Gly
                                                    10
              Ala Glu Xxx Gly Phe Pro Pro Lys Pro Phe Val Asp Trp Phe Cys
                               20
                                                    25
                                                                          30
              Gly Gly Phe Gln Tyr Gln Val Asp His His Leu Phe Pro Ser Leu
     25
                                                     40
              Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val Glu Ser Phe
(T
                                50
                                                     55
             Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu Val Asp
                                65
                                                     70
    30
             Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly Glu
                               65
                                                     70
              Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met
                                80
    35
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    40
              (2) INFORMATION FOR SEQ ID NO:23:
                   (i) SEQUENCE CHARACTERISTICS:
                        (A) LENGTH: 520 nucleic acids
                        (B) TYPE: amino acid
    45
                        (C) STRANDEDNESS: not relevant
                        (D) TOPOLOGY: linear
                  (ii) MOLECULE TYPE: nucleic acid
    50
                  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
             GGATGGAGTT CGTCTGGATC GCTGTGCGCT ACGCGACGTG GTTTAAGCGT CATGGGTGCG
             CTTGGGTACA CGCCGGGGCA GTCGTTGGGC ATGTACTTGT GCGCCTTTGG TCTCGGCTGC
    55
                                                                                     120
             ATTTACATTT TTCTGCAGTT CGCCGTAAGT CACACCCATT TGCCCGTGAG CAACCCGGAG
                                                                                     180
             GATCAGCTGC ATTGGCTCGA GTACGCGCGG ACCACACTGT GAACATCAGC ACCAAGTCGT
                                                                                     240
             GGTTTGTCAC ATGGTGGATG TCGAACCTCA ACTTTCAGAT CGAGCACCAC CTTTTCCCCA CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCGCGCGT CGAGGCCCTC TTCAAGCGCC
                                                                                     300
             ACGGTCTCCC TTACTACGAC ATGCCCTACA CGAGCGCCGT CTCCACCACC TTTGCCAACC
                                                                                     420
    60
             TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAGCGCGA CTAGCCTCTT TTCCTAGACC
                                                                                     480
             TTAATTCCCC ACCCCACCC ATGTTCTGTC TTCCTCCCGC
                                                                                     520
             (2) INFORMATION FOR SEQ ID NO:24:
  -- 65
                   (i) SEQUENCE CHARACTERISTICS:
```

```
(A) LENGTH: 153 amino acids
                       (B) TYPE: amino acid
                       (C) STRANDEDNESS: not relevant
                       (D) TOPOLOGY: linear
    5
                (ii) MOLECULE TYPE: peptide
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
   10
            Met Glu Phe Val Trp Ile Ala Val Arg Tyr Ala Thr Trp Phe Lys
                                                  10
            Arg His Gly Cys Ala Trp Val His Ala Gly Ala Val Val Gly His
                             20
                                                  25
   15
            Val Leu Val Arg Leu Trp Ser Arg Leu His Leu His Phe Ser Ala
                              35
            Val Arg Arg Lys Ser His Pro Phe Ala Arg Glu Gln Pro Gly Gly
                              50
                                                                       60
            Ser Ala Ala Leu Ala Arg Val Arg Ala Asp His Thr Val Asn Ile
   20
                                                  70
            Ser Thr Lys Ser Trp Phe Val Thr Trp Trp Met Ser Asn Leu Asn
                                                  85
            Phe Gln Ile Glu His His Leu Phe Pro Thr Ala Pro Gln Phe Arg
                              95
                                                 100 .
   25
            Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu Phe Lys Arg His
                             110
                                                 115
                                                                      120
i, Fi
            Gly Leu Pro Tyr Tyr Asp Met Pro Tyr Thr Ser Ala Val Ser Thr
                             125
                                                 130
            Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly Asp Ala
   30
                             140
                                                 145
            Lys Arg Asp
IJ
£i
   35
            (2) INFORMATION FOR SEQ ID NO:25:
ijŌ
(i) SEQUENCE CHARACTERISTICS:
                       (A) LENGTH: 420 nucleic acids
                       (B) TYPE: nucleic acid
   40
                       (C) STRANDEDNESS: not relevant
                       (D) TOPOLOGY: linear
                (ii) MOLECULE TYPE: nucleic acid
   45
                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
            ACGCGTCCGC CCACGCGTCC GCCGCGAGCA ACTCATCAAG GAAGGCTACT TTGACCCCTC
                                                                                   60
            GCTCCCGCAC ATGACGTACC GCGTGGTCGA GATTGTTGTT CTCTTCGTGC TTTCCTTTTG
                                                                                  120
   50
            GCTGATGGGT CAGTCTTCAC CCCTCGCGCT CGCTCTCGGC ATTGTCGTCA GCGGCATCTC
                                                                                  180
            TCAGGGTCGC TGCGGCTGGG TAATGCATGA GATGGGCCAT GGGTCGTTCA CTGGTGTCAT
                                                                                  240
            TTGGCTTGAC GACCGGTTGT GCGAGTTCTT TTACGGCGTT GGTTGTGGCA TGAGCGGTCA
                                                                                  300
            TTACTGGAAA AACCAGCACA GCAAACACCA CGCAGCGCCA AACCGGCTCG AGCACGATGT
                                                                                  360
            AGATCTCAAC ACCTTGCCAT TGGTGGCCTT CAACGAGCGC GTCGTGCGCA AGGTCCGACC
                                                                                  420
   55
            (2) INFORMATION FOR SEQ ID NO:26:
   60
                  (i) SEQUENCE CHARACTERISTICS:
                       (A) LENGTH: 125 amino acids
                       (B) TYPE: amino acid
                       (C) STRANDEDNESS: not relevant
                       (D) TOPOLOGY: linear
  --65
                 (ii) MOLECULE TYPE: peptide
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

	5	Arg Val Arg Pro Arg Val Arg Arg Glu Gln Leu Ile Lys Glu Gly	
		Tyr Phe Asp Pro Ser Leu Pro His Met Thr Tyr Arg Val Val Glu	
	10	20 25 30 Ile Val Val Leu Phe Val Leu Ser Phe Trp Leu Met Gly Gln Ser	
	10	35 40 45 Ser Pro Leu Ala Leu Gly Ile Val Val Ser Gly Ile Ser	
		50 55 60 Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly Ser	
	15	65 70 75	
		Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Leu Cys Glu Phe Phe 65 70 75	
		Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln 80 85 90	
	20	His Ser Lys His His Ala Ala Pro Asn Arg Leu Glu His Asp Val 95 100 105	
		Asp Leu Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val	
Q		Arg Lys Val Arg Pro 125 120	
	25		
'n		(2) INFORMATION FOR SEQ ID NO:27:	
`	20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 1219 base pairs	
t:⊒² Î:≛	30	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
ĻŲ		(D) TOPOLOGY: linear	
!: !:]	35	(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2692004)	
C	-		
IJ In		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
	40	GCACGCCGAC CGGCGCCGGG AGATCCTGGC AAAGTATCCA GAGATAAAGT CCTTGATGAA	60
٠ <u>.</u>]		ACCTGATCCC AATTTGATAT GGATTATAAT TATCATCCTT CTCACCCTT	
		TTACATAGTA AAAGACTTGG ACTGGAAATC CCTGATATTT CCCCCCTATA	120
	45		180
			240
	50		300
	50		360
			420
	55	AAAGTTTATA TGGGTTATTC TTCAGCCTCT CTTTTATGCC TTTCGACCTC TGTTCATCAA	480
		CCCCAAACCA ATTACGTATC TGGAAGTTAT CAATACCGTG GCACAGGTCA CTTTTGACAT	540
		TTTAATTTAT TACTTTTTGG GAATTAAATC CTTACTCTAC	600
	60	TGGCCTGGGT TTGCACCCAA TTTCTGCACA TTTTTATATAGG	660
		GGGTCATGAA ACTTACTCAT ATTATCCCCC TCTCAATTTA	
		TCATAATGAA CATCATGATT TCCCCAACAT TCCTCCAAAA ACTGTTTCCA	720
7	65		780
		AATAGCAGCT GAATACTATG ACAACCTCCC TCACTACAAT TCCTGGATAA AAGTACTGTA	840

		TOATTTTOTO ATGGATGATA CAATAAGTCC CTACTCAAGA ATGAAGAGGC ACCAAAAAGG	900
	5	AGAGATGGTG CTGGAGTAAA TATCATTAGT GCCAAAGGGA TTCTTCTCCA AAACTTTAGA	960
	3	TGATAAAATG GAATTTTTGC ATTATTAAAC TTGAGACCAG TGATGCTCAG AAGCTCCCCT	1020
		GGCACAATTT CAGAGTAAGA GCTCGGTGAT ACCAAGAAGT GAATCTGGCT TTTAAACAGT	1080
	10	CAGCCTGACT CTGTACTGCT CAGTTTCACT CACAGGAAAC TTGTGACTTG TGTATTATCG	1140
		TCATTGAGGA TGTTTCACTC ATGTCTGTCA TTTTATAAGC ATATCATTTA AAAAGCTTCT	1200
	15	AAAAAGCTAT TTCGCCAGG	1219
		(2) INFORMATION FOR SEQ ID NO:28:	
	20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 655 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
Ē., I.J	25	(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2153526)	
LINE THE THE	30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
. S.	30	TTACCTTCTA CGTCCGCTTC TTCCTCACTT ATGTGCCACT ATTGGGGCTG AAAGCTTCCT	60
í		GGGCCTTTTC TTCATAGTCA GGTTCCTGGA AAGCAACTGG TTTGTGTGGG TGACACAGAT	120
0	35	GAACCATATT CCCATGCACA TTGATCATGA CCGGAACATG GACTGGGTTT CCACCCAGCT	180
		CCAGGCCACA TGCAATGTCC ACAAGTCTGC CTTCAATGAC TGGTTCAGTG GACACCTCAA	240
Hall Hall Land Hall	40	CTTCCAGATT GAGCACCATC TTTTTCCCAC GATGCCTCGA CACAATTACC ACAAAGTGGC	300
F		TCCCCTGGTG CAGTCCTTGT GTGCCAAGCA TGGCATAGAG TACCAGTCCA AGCCCCTGCT	360
		GTCAGCCTTC GCCGACATCA TCCACTCACT AAAGGAGTCA GGGCAGCTCT GGCTAGATGC	420
	45	CTATCTTCAC CAATAACAAC AGCCACCCTG CCCAGTCTGG AAGAAGAGGA GGAAGACTCT	480
		GGAGCCAAGG CAGAGGGGAG CTTGAGGGGAC AATGCCACTA TAGTTTAATA CTCAGAGGGG	540
	50	GTTGGGTTTG GGGACATAAA GCCTCTGACT CAAACTCCTC CCTTTTATCT TCTAGCCACA	600
		GTTCTAAGAC CCAAAGTGGG GGGTGGACAC AGAAGTCCCT AGGAGGGAAG GAGCT	655
	55	(2) INFORMATION FOR SEQ ID NO:29:	
	60	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 304 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3506132)	
	₹5.	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
	•	GTCTTTTACT TTGGCAATGG CTGGATTCCT ACCCTCATCA CGGCCTTTGT CCTTGCTACC	60

		TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA	120
	5	CCCAAGTGGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC	180
		AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT	240
		CCCGATGTGA ACATGCTGCA CGTGTTTGTT CTGGGCGAAT GGCAGCCCAT CGAGTACGGC	300
	10	AAGA	304
		(2) INFORMATION FOR SEQ ID NO:30:	
	15	(i) SEQUENCE CHARACTERISTICS:	
	20	(A) LENGTH: 918 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	20	(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3854933)	
: = : :=		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
	25	CAGGGACCTA CCCCGCGCTA CTTCACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCGAG	60
		GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT	120
	30	CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTTGTG	180
		GCCTTCCACA TCAACAAGGG CCTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA	240
:		CTGTCTCCAG AGCAGCCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC	300
	35	CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC	360
: # <u>'</u>		CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGCAG CCTGGCTCAC CCTTTGGGTC	420
 J	10	TTTGGGACGT CCTTTTTGCC CTTCCTCCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGGCC	480
		CAGGCTGGCT GGCTGCAGCA TGACTTTGGG CACCTGTCGG TCTTCAGCAC CTCAAAGTGG	540
		AACCATCTGC TACATCATTT TGTGATTGGC CACCTGAAGG GGGCCCCCGC CAGTTGGTGG	600
4	15	AACCACATGC ACTTCCAGCA CCATGCCAAG CCCAACTGCT TCCGCAAAGA CCCAGACATC	660
		AACATGCATC CCTTCTTCTT TGCCTTGGGG AAGATCCTCT CTGTGGAGCT TGGGAAACAG	720
5	50	AAGAAAAAA ATATGCCGTA CAACCACCAG CACARATACT TCTTCCTAAT TGGGCCCCCA	780
		GCCTTGCTGC CTCTCTACTT CCAGTGGTAT ATTTTCTATT TTGTTATCCA GCGAAAGAAG	840
		TGGGTGGACT TGGCCTGGAT CAGCAAACAG GAATACGATG AAGCCGGGCT TCCATTGTCC	900
5	55	ACCGCAAATG CTTCTAAA	918
		(2) INFORMATION FOR SEQ ID NO:31:	
6	50	(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 1686 base pairs (B) TYPE: nucleic acid	
€	55	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
		(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2511785)	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

	5	GCCACTTAAA	GGGTGCCTCT	GCCAACTGGT	GGAATCATCG	CCACTTCCAG	CACCACGCCA	60
		AGCCTAACAT	CTTCCACAAG	GATCCCGATG	TGAACATGCT	GCACGTGTTT	GTTCTGGGCG	120
	10	AATGGCAGCC	CATCGAGTAC	GGCAAGAAGA	AGCTGAAATA	CCTGCCCTAC	AATCACCAGC	180
		ACGAATACTT	CTTCCTGATT	GGGCCGCCGC	TGCTCATCCC	CATGTATTTC	CAGTACCAGA	240
		TCATCATGAC	CATGATCGTC	CATAAGAACT	GGGTGGACCT	GGCCTGGGCC	GTCAGCTACT	300
	15	ACATCCGGTT	CTTCATCACC	TACATCCCTT	TCTACGGCAT	CCTGGGAGCC	CTCCTTTTCC	360
		TCAACTTCAT	CAGGTTCCTG	GAGAGCCACT	GGTTTGTGTG	GGTCACACAG	ATGAATCACA	420
	20	TCGTCATGGA	GATTGACCAG	GAGGCCTACC	GTGACTGGTT	CAGTAGCCAG	CTGACAGCCA	480
		CCTGCAACGT	GGAGCAGTCC	TTCTTCAACG	ACTGGTTCAG	TGGACACCTT	AACTTCCAGA	540
3		TTGAGCACCA	CCTCTTCCCC	ACCATGCCCC	GGCACAACTT	ACACAAGATC	GCCCCGCTGG	600
J	25	TGAAGTCTCT	ATGTGCCAAG	CATGGCATTG	AATACCAGGA	GAAGCCGCTA	CTGAGGGCCC	660
The		TGCTGGACAT	CATCAGGTCC	CTGAAGAAGT	CTGGGAAGCT	GTGGCTGGAC	GCCTACCTTC	720
1n	30	ACAAATGAAG	CCACAGCCCC	CGGGACACCG	TGGGGAAGGG	GTGCAGGTGG	GGTGATGGCC	780
É		AGAGGAATGA	TGGGCTTTTG	TTCTGAGGGG	TGTCCGAGAG	GCTGGTGTAT	GCACTGCTCA	840
er.		CGGACCCCAT	GTTGGATCTT	TCTCCCTTTC	TCCTCTCCTT	TTTCTCTTCA	CATCTCCCCC	900
7 5	35	ATAGCACCCT	GCCCTCATGG	GAÇCTGCCCT	CCCTCAGCCG	TCAGCCATCA	GCCATGGCCC	960
**************************************		TCCCAGTGCC	TCCTAGCCCC	TTCTTCCAAG	GAGCAGAGAG	GTGGCCACCG	GGGGTGGCTC	1020
E., H., II.	40	TGTCCTACCT	CCACTCTCTG	CCCCTAAAGA	TGGGAGGAGA	CCAGCGGTCC	ATGGGTCTGG	1080
#		CCTGTGAGTC	TCCCCTTGCA	GCCTGGTCAC	TAGGCATCAC	CCCCGCTTTG	GTTCTTCAGA	1140
		TGCTCTTGGG	GTTCATAGGG	GCAGGTCCTA	GTCGGGCAGG	GCCCCTGACC	CTCCCGGCCT	1200
	45	GGCTTCACTC	TCCCTGACGG	CTGCCATTGG	TCCACCCTTT	CATAGAGAGG	CCTGCTTTGT	1260
		TACAAAGCTC	GGGTCTCCCT	CCTGCAGCTC	GGTTAAGTAC	CCGAGGCCTC	TCTTAAGATG	1320
	50	TCCAGGGCCC	CAGGCCCGCG	GGCACAGCCA	GCCCAAACCT	TGGGCCCTGG	AAGAGTCCTC	1380
		CACCCCATCA	CTAGAGTGCT	CTGACCCTGG	GCTTTCACGG	GCCCCATTCC	ACCGCCTCCC	1440
		CAACTTGAGC	CTGTGACCTT	GGGACCAAAG	GGGGAGTCCC	TCGTCTCTTG	TGACTCAGCA	1500
	55	GAGGCAGTGG	CCACGTTCAG	GGAGGGGCCG	GCTGGCCTGG	AGGCTCAGCC	CACCCTCCAG	1560
		CTTTTCCTCA	GGGTGTCCTG	AGGTCCAAGA	TTCTGGAGCA	ATCTGACCCT	TCTCCAAAGG	1620
	60	CTCTGTTATC	AGCTGGGCAG	TGCCAGCCAA	TCCCTGGCCA	TTTGGCCCCA	GGGGACGTGG	1680
		GCCCTG						1686

(2) INFORMATION FOR SEQ ID NO:32:

-65

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1843 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: other nucleic acid (Contig 2535)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

10 GTCTTTTACT TTGGCAATGG CTGGATTCCT ACCCTCATCA CGGCCTTTGT CCTTGCTACC 60 TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA 120 15 CCCAAGTGGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC 180 AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT 240 CCCGATGTGA ACATGCTGCA CGTGTTTGTT CTGGGCGAAT GGCAGCCCAT CGAGTACGGC 300 20 AAGAAGAAGC TGAAATACCT GCCCTACAAT CACCAGCACG AATACTTCTT CCTGATTGGG 360 CCGCCGCTGC TCATCCCCAT GTATTTCCAG TACCAGATCA TCATGACCAT GATCGTCCAT 420 25 AAGAACTGGG TGGACCTGGC CTGGGCCGTC AGCTACTACA TCCGGTTCTT CATCACCTAC 480 ĩ.ĥ ATCCCTTTCT ACGGCATCCT GGGAGCCCTC CTTTTCCTCA ACTTCATCAG GTTCCTGGAG 540 اً ۽ ٿ AGCCACTGGT TTGTGTGGGT CACACAGATG AATCACATCG TCATGGAGAT TGACCAGGAG 600 30 <u>.</u> GCCTACCGTG ACTGGTTCAG TAGCCAGCTG ACAGCCACCT GCAACGTGGA GCAGTCCTTC 660 Į, J TTCAACGACT GGTTCAGTGG ACACCTTAAC TTCCAGATTG AGCACCACCT CTTCCCCACC £: 720 ij 35 ATGCCCCGGC ACAACTTACA CAAGATCGCC CCGCTGGTGA AGTCTCTATG TGCCAAGCAT 780 ľŌ GGCATTGAAT ACCAGGAGAA GCCGCTACTG AGGGCCCTGC TGGACATCAT CAGGTCCCTG 840 Į,Tį AAGAAGTCTG GGAAGCTGTG GCTGGACGCC TACCTTCACA AATGAAGCCA CAGCCCCCGG 900 40 GACACCGTGG GGAAGGGGTG CAGGTGGGGT GATGGCCAGA GGAATGATGG GCTTTTGTTC 960 TGAGGGGTGT CCGAGAGGCT GGTGTATGCA CTGCTCACGG ACCCCATGTT GGATCTTTCT 1020 45 CCCTTTCTCC TCTCCTTTTT CTCTTCACAT CTCCCCCATA GCACCCTGCC CTCATGGGAC 1080 CTGCCCTCCC TCAGCCGTCA GCCATCAGCC ATGGCCCTCC CAGTGCCTCC TAGCCCCTTC 1140 TTCCAAGGAG CAGAGAGGTG GCCACCGGGG GTGGCTCTGT CCTACCTCCA CTCTCTGCCC 1200 50 CTAAAGATGG GAGGAGACCA GCGGTCCATG GGTCTGGCCT GTGAGTCTCC CCTTGCAGCC 1260 TGGTCACTAG GCATCACCCC CGCTTTGGTT CTTCAGATGC TCTTGGGGTT CATAGGGGCA 1320 55 GGTCCTAGTC GGGCAGGGCC CCTGACCCTC CCGGCCTGGC TTCACTCTCC CTGACGGCTG CCATTGGTCC ACCCTTTCAT AGAGAGGCCT GCTTTGTTAC AAAGCTCGGG TCTCCCTCCT 1440 GCAGCTCGGT TAAGTACCCG AGGCCTCTCT TAAGATGTCC AGGGCCCCAG GCCCGCGGGC 1500 60 ACAGCCAGCC CAAACCTTGG GCCCTGGAAG AGTCCTCCAC CCCATCACTA GAGTGCTCTG 1560 ACCCTGGGCT TTCACGGGCC CCATTCCACC GCCTCCCCAA CTTGAGCCTG TGACCTTGGG 1620 -65 ACCAAAGGGG GAGTCCCTCG TCTCTTGTGA CTCAGCAGAG GCAGTGGCCA CGTTCAGGGA 1680

		GGGGCCGGCT	GGCCTGGAGG	CTCAGCCCAC	CCTCCAGCTT	TTCCTCAGGG	TGTCCTGAGG	1740
		TCCAAGATTC	TGGAGCAATC	TGACCCTTCT	CCAAAGGCTC	TGTTATCAGC	TGGGCAGTGC	1800
	5	CAGCCAATCC	CTGGCCATTT	GGCCCCAGGG	GACGTGGGCC	CTG		1843
		(2) INFORMA	TION FOR SE	Q ID NO:33:				
	10	(A) LENGTH: (B) TYPE: nu	NESS: sing	pairs			
	15				oleje acid ((Editod Cont	ig 253538a)	
				RIPTION: SE			ilg 253538a)	
	20			CTTCACCTGG			ACCCTCCCAC	60
				CCGTAAGGTG				
¥ 16J				CAGCCACTAC				120
	25			CCTTGTGAAG				180
								240
B. 18.43 A	30			CTTTGAGCCC				300
fi Pr	50			GGAGCGGATG				360
				CTTGCTGCTG				420
1H 4H 4H 4H 4H	35			CTTCCTCCTC				480
14.34				ACATGATTAT				540
	40			ATTCGTCATT				600
11,1	40			GCACCACGCC				660
				TGTTCTGGGC				720
	45			CAATCACCAG				780
		CTGCTCATCC	CCATGTATTT	CCAGTACCAG	ATCATCATGA	CCATGATCGT	CCATAAGAAC	840
		TGGGTGGACC	TGGCCTGGGC	CGTCAGCTAC	TACATCCGGT	TCTTCATCAC	CTACATCCCT	900
	50	TTCTACGGCA	TCCTGGGAGC	CCTCCTTTTC	CTCAACTTCA	TCAGGTTCCT	GGAGAGCCAC	960
		TGGTTTGTGT	GGGTCACACA	GATGAATCAC	ATCGTCATGG	AGATTGACCA	GGAGGCCTAC	1020
	55	CGTGACTGGT	TCAGTAGCCA	GCTGACAGCC	ACCTGCAACG	TGGAGCAGTC	CTTCTTCAAC	1080
		GACTGGTTCA	GTGGACACCT	TAACTTCCAG	ATTGAGCACC	ACCTCTTCCC	CACCATGCCC	1140
		CGGCACAACT	TACACAAGAT	CGCCCCGCTG	GTGAAGTCTC	TATGTGCCAA	GCATGGCATT	1200
	60	GAATACCAGG	AGAAGCCGCT	ACTGAGGGCC	CTGCTGGACA	TCATCAGGTC	CCTGAAGAAG	1260
		TCTGGGAAGC	TGTGGCTGGA	CGCCTACCTT	CACAAATGAA	GCCACAGCCC	CCGGGACACC	1320
	-65	GTGGGGAAGG	GGTGCAGGTG	GGGTGATGGC	CAGAGGAATG	ATGGGCTTTT	GTTCTGAGGG	1380
	<i>02.</i>						TTCTCCCTTT	1440

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CTCCTCTCCT TTTTCTCTTC ACATCTCCCC CATAGCACCC TGCCCTCATG GGACCTGCCC
            TCCCTCAGCC GTCAGCCATC AGCCATGGCC CTCCCAGTGC CTCCTAGCCC CTTCTTCCAA
                                                                                 1560
    5
            GGAGCAGAGA GGTGGCCACC GGGGGTGGCT CTGTCCTACC TCCACTCTCT GCCCCTAAAG
                                                                                 1620
            ATGGGAGGAG ACCAGCGGTC CATGGGTCTG GCCTGTGAGT CTCCCCTTGC AGCCTGGTCA
                                                                                 1680
   10
            CTAGGCATCA CCCCCGCTTT GGTTCTTCAG ATGCTCTTGG GGTTCATAGG GGCAGGTCCT
                                                                                 1740
            AGTCGGGCAG GGCCCCTGAC CCTCCCGGCC TGGCTTCACT CTCCCTGACG GCTGCCATTG
            GTCCACCCTT TCATAGAGAG GCCTGCTTTG TTACAAAGCT CGGGTCTCCC TCCTGCAGCT
                                                                                 1860
   15
            CGGTTAAGTA CCCGAGGCCT CTCTTAAGAT GTCCAGGGCC CCAGGCCCGC GGGCACAGCC
                                                                                 1920
            AGCCCAAACC TTGGGCCCTG GAAGAGTCCT CCACCCCATC ACTAGAGTGC TCTGACCCTG
                                                                                1980
   20
            GGCTTTCACG GGCCCCATTC CACCGCCTCC CCAACTTGAG CCTGTGACCT TGGGACCAAA
                                                                                 2040
            GGGGGAGTCC CTCGTCTCTT GTGACTCAGC AGAGGCAGTG GCCACGTTCA GGGAGGGGCC
                                                                                 2100
            GGCTGGCCTG GAGGCTCAGC CCACCCTCCA GCTTTTCCTC AGGGTGTCCT GAGGTCCAAG
   25
            ATTCTGGAGC AATCTGACCC TTCTCCAAAG GCTCTGTTAT CAGCTGGGCA GTGCCAGCCA
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اً. با
            ATCCCTGGCC ATTTGGCCCC AGGGGACGTG GGCCCTG
                                                                                 2257
30
ļ. <u>4</u>
            (2) INFORMATION FOR SEQ ID NO:34:
ĮŲ
                  (i) SEQUENCE CHARACTERISTICS:
£j
                       (A) LENGTH: 411 amino acids
35
                       (B) TYPE: amino acid
                       (C) STRANDEDNESS: single
13
                       (D) TOPOLOGY: linear
l,f
                (ii) MOLECULE TYPE: amino acid (Translation of Contig 2692004)
   40
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
            His Ala Asp Arg Arg Glu Ile Leu Ala Lys Tyr Pro Glu Ile
   45
                                                 10
            Lys Ser Leu Met Lys Pro Asp Pro Asn Leu Ile Trp Ile Ile Ile
                                                  25
            Met Met Val Leu Thr Gln Leu Gly Ala Phe Tyr Ile Val Lys Asp
                              35
                                                  40
   50
            Leu Asp Trp Lys Trp Val Ile Phe Gly Ala Tyr Ala Phe Gly Ser
                              50
                                                  55
            Cys Ile Asn His Ser Met Thr Leu Ala Ile His Glu Ile Ala His
                              65
                                                  70
            Asn Ala Ala Phe Gly Asn Cys Lys Ala Met Trp Asn Arg Trp Phe
   55
                             80
                                                  85
            Gly Met Phe Ala Asn Leu Pro Ile Gly Ile Pro Tyr Ser Ile Ser
                             95
                                                 100
                                                                      105
            Phe Lys Arg Tyr His Met Asp His His Arg Tyr Leu Gly Ala Asp
                             110
                                                 115
   60
            Gly Val Asp Val Asp Ile Pro Thr Asp Phe Glu Gly Trp Phe Phe
                            125
                                                 130
                                                                      135
            Cys Thr Ala Phe Arg Lys Phe Ile Trp Val Ile Leu Gln Pro Leu
                            140
                                                 145
                                                                      150
            Phe Tyr Ala Phe Arg Pro Leu Phe Ile Asn Pro Lys Pro Ile Thr
  65
                             155
                                                 160
            Tyr Leu Glu Val Ile Asn Thr Val Ala Gln Val Thr Phe Asp Ile
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170
                                                 175
            Leu Ile Tyr Tyr Phe Leu Gly Ile Lys Ser Leu Val Tyr Met Leu
                            185
                                                 190
            Ala Ala Ser Leu Leu Gly Leu Gly Leu His Pro Ile Ser Gly His
    5
                            200
                                                 205
            Phe Ile Ala Glu His Tyr Met Phe Leu Lys Gly His Glu Thr Tyr
                            215
                                                 220
            Ser Tyr Tyr Gly Pro Leu Asn Leu Leu Thr Phe Asn Val Gly Tyr
                            230
                                                 235
   10
            His Asn Glu His His Asp Phe Pro Asn Ile Pro Gly Lys Ser Leu
                                                 250
            Pro Leu Val Arg Lys Ile Ala Ala Glu Tyr Tyr Asp Asn Leu Pro
                            260
                                                 265
            His Tyr Asn Ser Trp Ile Lys Val Leu Tyr Asp Phe Val Met Asp
   15
                            275
                                                 280
            Asp Thr Ile Ser Pro Tyr Ser Arg Met Lys Arg His Gln Lys Gly
                            290
                                                 295
            Glu Met Val Leu Glu *** Ile Ser Leu Val Pro Lys Gly Phe Phe
                            305
                                                 310
   20
            Ser Lys Thr Leu Asp Asp Lys Met Glu Phe Leu His Tyr *** Thr
                            320
                                                 325
                                                                     330
            *** Asp Gln *** Cys Ser Glu Ala Pro Leu Ala Gln Phe Gln Ser
                            335
                                                 340
            Lys Ser Ser Val Ile Pro Arg Ser Glu Ser Gly Phe *** Thr Val
   25
                            350
                                                 355
            Ser Leu Thr Leu Tyr Cys Ser Val Ser Leu Thr Gly Asn Leu ***
                            365
                                                 370
                                                                     375
            Leu Val Tyr Tyr Arg His *** Gly Cys Phe Thr His Val Cys His
                            380
                                                 385
            Phe Ile Ser Ile Ser Phe Lys Lys Leu Leu Lys Ser Tyr Phe Ala
                                                 405
            (2) INFORMATION FOR SEQ ID NO:35:
                 (i) SEQUENCE CHARACTERISTICS:
13
                      (A) LENGTH: 218 amino acids
Į,
                      (B) TYPE: amino acid
                      (C) STRANDEDNESS: single
  40
                      (D) TOPOLOGY: linear
                (ii) MOLECULE TYPE: amino acid (Translation of Contig 2153526)
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
   45
            Tyr Leu Leu Arg Pro Leu Leu Pro His Leu Cys Ala Thr Ile Gly
                                                 10
            Ala Glu Ser Phe Leu Gly Leu Phe Phe Ile Val Arg Phe Leu Glu
   50
                             20
                                                  25
            Ser Asn Trp Phe Val Trp Val Thr Gln Met Asn His Ile Pro Met
                             35
                                                  40
            His Ile Asp His Asp Arg Asn Met Asp Trp Val Ser Thr Gln Leu
                             50
                                                  55
   55
            Gln Ala Thr Cys Asn Val His Lys Ser Ala Phe Asn Asp Trp Phe
                              65
                                                  70
            Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr
                              80
            Met Pro Arg His Asn Tyr His Lys Val Ala Pro Leu Val Gln Ser
   60
                             95
                                                 100
            Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser Lys Pro Leu Leu
                            110
                                                 115
            Ser Ala Phe Ala Asp Ile Ile His Ser Leu Lys Glu S r Gly Gln
                            125
                                                 130
  <del>-</del>65.
            Leu Trp Leu Asp Ala Tyr Leu His Gln *** Gln Gln Pro Pro Cys
                            140
```

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Pro Val Trp Lys Lys Arg Arg Lys Thr Leu Glu Pro Arg Gln Arg
                              155
                                                  160
             Gly Ala *** Gly Thr Met Pro Leu *** Phe Asn Thr Gln Arg Gly
                              170
                                                  175
                                                                       180
     5
             Leu Gly Leu Gly Thr *** Ser Leu *** Leu Lys Leu Leu Pro Phe
                             185
                                                  190
             Ile Phe *** Pro Gln Phe *** Asp Pro Lys Trp Gly Val Asp Thr
                             200
                                                  205
             Glu Val Pro Arg Arg Glu Gly Ala
    10
                             215
             (2) INFORMATION FOR SEQ ID NO:36:
    15
                  (i) SEQUENCE CHARACTERISTICS:
                       (A) LENGTH: 86 amino acids
                        (B) TYPE: amino acid
                       (C) STRANDEDNESS: single
    20
                       (D) TOPOLOGY: linear
                 (ii) MOLECULE TYPE: amino acid (Translation of Contig 3506132)
                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
    25
(fi
             Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala
    30
             Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His
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             Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His
Đ;
                              35
                                                   40
             Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala
                              50
                                                   55
ij
             Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn
j
                              65
                                                   70
             Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Xxx
                              80
    40
             (2) INFORMATION FOR SEQ ID NO:37:
    45
                  (i) SEQUENCE CHARACTERISTICS:
                       (A) LENGTH: 306 amino acids
                       (B) TYPE: amino acid
                       (C) STRANDEDNESS: single
                       (D) TOPOLOGY: linear
    50
                 (ii) MOLECULE TYPE: amino acid (Translation of Contig 3854933)
                 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
    55
            Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln
            Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val
                              20
                                                   25
                                                                       30
   60
            Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg
                              35
                                                   40
            Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val
                              50
                                                   55
            Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser
  --65
                              65
                                                   70
            Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro
```

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80
            Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala
                              95
                                                 100
            Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe
    5
                             110
                                                 115
                                                                      120
            Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp
                             125
                                                 130
                                                                      135
            Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu
                             140
                                                 145
   10
            Cys Ala Val Leu Leu Ser Ala Val Gln Ala Gln Ala Gly Trp Leu
                             155
                                                 160
            Gln His Asp Phe Gly His Leu Ser Val Phe Ser Thr Ser Lys Trp
                            170
                                                 175
            Asn His Leu Leu His His Phe Val Ile Gly His Leu Lys Gly Ala
   15
                            185
                                                 190
            Pro Ala Ser Trp Trp Asn His Met His Phe Gln His His Ala Lys
                            200
                                                 205
                                                                      210
            Pro Asn Cys Phe Arg Lys Asp Pro Asp Ile Asn Met His Pro Phe
                             215
                                                 220
                                                                      225
   20
            Phe Phe Ala Leu Gly Lys Ile Leu Ser Val Glu Leu Gly Lys Gln
                             230
                                                 235
            Lys Lys Lys Tyr Met Pro Tyr Asn His Gln His Xxx Tyr Phe Phe
                             245
                                                 250
                                                                      255
            Leu Ile Gly Pro Pro Ala Leu Leu Pro Leu Tyr Phe Gln Trp Tyr
   25
                            260
                                                 265
                                                                      270
            Ile Phe Tyr Phe Val Ile Gln Arg Lys Lys Trp Val Asp Leu Ala
ľΠ
                             275
                                                 280
            Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ala Gly Leu Pro Leu Ser
                             290
                                                 295
   30
            Thr Ala Asn Ala Ser Lys
ļ: ±
                             305
IJ
21
            (2) INFORMATION FOR SEQ ID NO:38:
   35
ľŌ
                  (i) SEQUENCE CHARACTERISTICS:
13
                       (A) LENGTH: 566 amino acids
                       (B) TYPE: amino acid
1,5
                       (C) STRANDEDNESS: single
   40
                       (D) TOPOLOGY: linear
                (ii) MOLECULE TYPE: amino acid (Translation of Contig 2511785)
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
   45
            His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn His Arg His Phe
                                                  10
            Gln His His Ala Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val
   50
                                                  25
            Asn Met Leu His Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu
                              35
                                                   40
            Tyr Gly Lys Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His
                              50
                                                  55
                                                                       60
   55
            Glu Tyr Phe Phe Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr
                              65
                                                  70
                                                                       75
            Phe Gln Tyr Gln Ile Ile Met Thr Met Ile Val His Lys Asn Trp
                              80
                                                  85
                                                                       90
            Val Asp Leu Ala Trp Ala Val Ser Tyr Tyr Ile Arg Phe Phe Ile
   60
                              95
                                                 100
            Thr Tyr Ile Pro Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe Leu
                             110
                                                 115
            Asn Phe Ile Arg Phe Leu Glu Ser His Trp Phe Val Trp Val Thr
                             125
                                                 130
  -65
            Gln Met Asn His Ile Val Met Glu Ile Asp Gln Glu Ala Tyr Arg
                                                 145
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		Asp	Trp	Phe	Ser	Ser	Gln	Leu	Thr	· Ala	Thr	Cvs	Den	Val	C1	Gln .
					Asn	TOO					160					1 6 5
	5					7,0					175					100
					Leu	702					190					105
					Leu	200					205					210
	10				Lys	213					220					225
					Lys	230					235					His
		Lys	***	Ser	His	Ser 245	Pro	Arg	Asp	Thr	Val 250	Gly	Lys	Gly	Cys	Arg
	15	Trp	Gly	Asp	Gly	Gln 260	Arg	Asn	Asp	Gly	Leu 265	Leu	Phe	***	Gly	
		Ser	Glu	Arg	Leu		Tyr	Ala	Leu	Leu	Thr	Asp	Pro	Met	Leu	270 Asp
	20	Leu	Ser	Pro	Phe		Leu	Ser	Phe	Phe	280 Ser	Ser	His	Leu	Pro	285 His
		Ser	Thr	Leu	Pro	Ser	Trp	Asp	Leu	Pro	295 Ser	Leu	Ser	Arg	Gln	300 Pro
P9					Ala	Leu					310					216
Ę,	25				Trp	Pro					325					222
[.J					Lys	333					34∩					245
, 7	• •				Pro	330					355					360
P. P.	30					303					370					375 Ser
Ų						300					385					200
# 1	35				Pro	400					405					410
(0					Leu	410					42n					405
					Gly	430					435					4 4 4
۱.5	40				Asp	440					45N					Ser
1,3		Pro				400					465					Ser
		Ala				4/3					His					
	45	Thr									Gly					
		Leu	***	Leu	Ser	Arg 505	Gly	Ser	Gly	His	Val	Gln	Gly	Gly	Ala	500 Gly
	50	Trp	Pro	Gly	Gly	Ser 520	Ala	His	Pro	Pro	510 Ala	Phe	Pro	Gln	Gly	515 Val
		Leu .	Arg	Ser	Lys	Ile	Leu	Glu	Gln	Ser	525 Asp	Pro	Ser	Pro	Lys	530 Ala
		Leu			Ala	Gly					540					
	55	Pro			Val	Gly					55 5					560
						565										
(2) INFORMATION FOR SEQ ID NO:39:																
	00			SEQ	UENC	Е СН	ARAC	TERI	STIC	s:						
				(A) LE	ngth	: 61	9 am	ino	acid	s					
(B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear																
				,,,	, 10	- 610	J	TTHE	αr							

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2535)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val Asn Met Leu His Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile Ile Met Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala Trp Ala Val (n Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu Ser His Trp Phe Val Trp Val Thr Gln Met Asn His Ile Val Met 1,4 Glu Ile Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr Cys Asn Val Glu Gln Ser Phe Phe Asn Asp Trp Phe ľ.Ģ Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr LF Met Pro Arg His Asn Leu His Lys Ile Ala Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Glu Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His Lys *** Ser His Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg Trp Gly Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe *** Gly Val Ser Glu Arg Leu Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp Leu Ser Pro Phe Leu Leu Ser Phe Phe Ser Ser His Leu Pro His Ser Thr Leu Pro Ser Trp Asp Leu Pro Ser Leu Ser Arg Gln Pro Ser Ala Met Ala Leu Pro Val Pro Pro Ser Pro Phe Phe Gln Gly Ala Glu Arg Trp Pro Pro Gly Val Ala Leu Ser Tyr Leu His Ser Leu Pro Leu Lys Met Gly Gly Asp Gln Arg Ser Met Gly Leu Ala Cys Glu Ser Pro Leu Ala Ala Trp Ser Leu Gly Ile Thr Pro Ala Leu Val Leu Gln Met Leu Leu ~65 Gly Phe Ile Gly Ala Gly Pro Ser Arg Ala Gly Pro Leu Thr Leu

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Pro Ala Trp Leu His Ser Pro *** Arg Leu Pro Leu Val His Pro
                            460
                                                465
            Phe Ile Glu Arg Pro Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro
                            475
    5
            Ala Ala Arg Leu Ser Thr Arg Gly Leu Ser *** Asp Val Gln Gly
                            490
                                                 495
                                                                     500
            Pro Arg Pro Ala Gly Thr Ala Ser Pro Asn Leu Gly Pro Trp Lys
                            505
                                                510
                                                                     515
            Ser Pro Pro Pro His His *** Ser Ala Leu Thr Leu Gly Phe His
   10
                            520
                                                525
            Gly Pro His Ser Thr Ala Ser Pro Thr *** Ala Cys Asp Leu Gly
                            535
                                                540
                                                                     545
            Thr Lys Gly Gly Val Pro Arg Leu Leu *** Leu Ser Arg Gly Ser
                            550
                                                 555
                                                                     560
   15
            Gly His Val Gln Gly Gly Ala Gly Trp Pro Gly Gly Ser Ala His
                            565
                                                570
            Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys Ile Leu Glu
                            580
                                                585
            Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala Gly Gln Cys
   20
                            595
                                                600
            Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val Gly Pro Xxx
                                                615
25
            (2) INFORMATION FOR SEQ ID NO:40:
i.T
                 (i) SEQUENCE CHARACTERISTICS:
                      (A) LENGTH: 757 amino acids
  30
                      (B) TYPE: amino acid
                      (C) STRANDEDNESS: single
Ų
                      (D) TOPOLOGY: linear
                (ii) MOLECULE TYPE: amino acid (Translation of Contig 253538a)
   35
                (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
Į,ſļ
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آياً 40
            Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln
           Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val
           Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg
                             35
                                                 40
   45
           Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val
                             50
                                                 55
           Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser
                             65
                                                 70
           Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro
   50
                             80
                                                 8.5
           Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala
                             95
                                                100
           Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe
                            110
                                                115
  55
           Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp
                            125
                                                130
           Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu
                            140
                                                145
                                                                     150
           Cys Ala Val Leu Leu Ser Ala Val Gln Gln Ala Gln Ala Gly Trp
  60
                            155
                                                160
           Leu Gln His Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys
                            170
                                                175
                                                                     180
           Trp Asn His Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly
                            185
                                                190
  65.
           Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln His His Ala
                            200
                                                205
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		Lys	Pro	Asn	Ile	Phe 215	His	Lys	Asp	Pro	Asp 220	Val	Asn	Met	Leu	His 225
						230					11e 235			Gly	_	Lys 240
	5	Lys	Leu	Lys	Tyr	Leu 245	Pro	Tyr	Asn	His	Gln 250	His	Glu	Tyr	Phe	Phe 255
		Leu	Ile	Gly	Pro	Pro 260	Leu	Leu	Ile	Pro		Tyr	Phe	Gln	Tyr	
1	0	Ile	Ile	Met	Thr	Met 275	Ile	Val	His	Lys	Asn 280	Trp	Val	Asp	Leu	
		Trp	Ala	Val	Ser	Tyr 290	Tyr	Ile	Arg	Phe	Phe 295	Ile	Thr	Tyr	Ile	Pro 300
	_					305					310			Phe		315
1	.5	Phe	Leu	Glu	Ser	His 320	Trp	Phe	Val	Trp	Val 325	Thr	Gln	Met	Asn	His 330
		Ile	Val	Met	Glu	Ile 335	qzA	Gln	Glu	Ala	Tyr 340	Arg	Asp	Trp	Phe	Ser 345
2	20	Ser	Gln	Leu	Thr	Ala 350	Thr	Cys	Asn	Val	Glu 355	Gln	Ser	Phe	Phe	Asn 360
						365					370			His		375
72	_					380					385			Ala		390
132	2.5					400					405			Gln		410
						415					420			Leu		425
D :	0					430					435			***		440
14 14						445					450			Gly		455
# #= _						460					465			Glu	-	470
(3 3 (0	15					475					480			Ser		485
						490					495			Thr		500
·34	10					505					510			Ala		515
-						520					525			Glu		530
						535					540			Pro		545
4	1 5					550					555			Glu		560
						565					570			Val		575
5	50					580					585			Ala		590
						595					600			Leu		605
,						610					615			Ser		620
3	55					625					630			Ser		635
						640					645			Asn		650
ć	50					655					660			Leu		Leu 665
						670					675			***		Cys 680
_4	. 					685					690			***		Ser
₹	55,_	Arg	Gly	Ser	Gly	His 700	Val	Gln	Gly	Gly	Ala 705	Gly	Trp	Pro	Gly	Gly 710

Ser Ala His Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys
715
720
725

Ile Leu Glu Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala
730
735
740

Gly Gln Cys Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val
745
755

Gly Pro Xxx

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SEQUENCE LISTING

5	(1) GENER	AL INFORMATION:
J		
	(1)	APPLICANT: KNUTZON, DEBORAH MURKERJI, PRADIP
1.0		HUANG, YUNG-SHENG
10		THURMOND, JENNIFER
		CHAUDHARY, SUNITA LEONARD, AMANDA
15	(ii)	TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS
13		OF BONG CHAIN FOLI-UNSATURATED FATTE ACIDS
	(iii)	NUMBER OF SEQUENCES: 40
	(iv)	CORRESPONDENCE ADDRESS:
20		(A) ADDRESSEE: LIMBACH AND LIMBACH LLP
		(B) STREET: 2001 FERRY BUILDING
		(C) CITY: SAN FRANCISCO (D) STATE: CA
		(E) COUNTRY: USA
25		(F) ZIP: 94111
	(v)	COMPUTER READABLE FORM:
		(A) MEDIUM TYPE: Floppy disk
30		(B) COMPUTER: IBM PC compatible
30		(C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: Microsoft Word
		(b) Softman income word
	(vi)	CURRENT APPLICATION DATA:
35		(A) APPLICATION NUMBER: (B) (B) FILING DATE:
		(C) CLASSIFICATION:
	(21111)	ATTORNEY/AGENT INFORMATION:
	(VIII)	(A) NAME: WARD, MICHAEL R.
40		(B) REGISTRATION NUMBER: 38,651
		(C) REFERENCE/DOCKET NUMBER: CGAB-210
	(ix)	TELECOMMUNICATION INFORMATION:
45		(A) TELEPHONE: (415) 433-4150
40		(B) TELEFAX: (415) 433-8716 (C) TELEX: N/A
	(2) INFOR	MATION FOR SEQ ID NO:1:
50		-
	(1)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 1617 base pairs
		(B) TYPE: nucleic acid
<i>5 5</i>		(C) STRANDEDNESS: single
55		(D) TOPOLOGY: linear
	(ii)	MOLECULE TYPE: other nucleic acid
60		
-		
	(xi)	SECULENCE DESCRIPTION: SEC ID NO.1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

-143-

	CGACACTCCT	TCCTTCTTCT	CACCCGTCCT	AGTCCCCTTC	AACCCCCCTC	TTTGACAAAG	60
	ACAACAAACC	ATGGCTGCTG	CTCCCAGTGT	GAGGACGTTT	ACTCGGGCCG	AGGTTTTGAA	120
5	TGCCGAGGCT	CTGAATGAGG	GCAAGAAGGA	TGCCGAGGCA	CCCTTCTTGA	TGATCATCGA	180
	CAACAAGGTG	TACGATGTCC	GCGAGTTCGT	CCCTGATCAT	CCCGGTGGAA	GTGTGATTCT	240
10	CACGCACGTT	GGCAAGGACG	GCACTGACGT	CTTTGACACT	TTTCACCCCG	AGGCTGCTTG	300
	GGAGACTCTT	GCCAACTTTT	ACGTTGGTGA	TATTGACGAG	AGCGACCGCG	ATATCAAGAA	360
	TGATGACTTT	GCGGCCGAGG	TCCGCAAGCT	GCGTACCTTG	TTCCAGTCTC	TTGGTTACTA	420
15	CGATTCTTCC	AAGGCATACT	ACGCCTTCAA	GGTCTCGTTC	AACCTCTGCA	TCTGGGGTTT	480
	GTCGACGGTC	ATTGTGGCCA	AGTGGGGCCA	GACCTCGACC	CTCGCCAACG	TGCTCTCGGC	540
20	TGCGCTTTTG	GGTCTGTTCT	GGCAGCAGTG	CGGATGGTTG	GCTCACGACT	TTTTGCATCA	600
	CCAGGTCTTC	CAGGACCGTT	TCTGGGGTGA	TCTTTTCGGC	GCCTTCTTGG	GAGGTGTCTG	660
	CCAGGGCTTC	TCGTCCTCGT	GGTGGAAGGA	CAAGCACAAC	ACTCACCACG	CCGCCCCAA	720
25	CGTCCACGGC	GAGGATCCCG	ACATTGACAC	CCACCCTCTG	TTGACCTGGA	GTGAGCATGC	780
	GTTGGAGATG	TTCTCGGATG	TCCCAGATGA	GGAGCTGACC	CGCATGTGGT	CGCGTTTCAT	840
30	GGTCCTGAAC	CAGACCTGGT	TTTACTTCCC	CATTCTCTCG	TTTGCCCGTC	TCTCCTGGTG	900
	CCTCCAGTCC	ATTCTCTTTG	TGCTGCCTAA	CGGTCAGGCC	CACAAGCCCT	CGGGCGCGCG	960
	TGTGCCCATC	TCGTTGGTCG	AGCAGCTGTC	GCTTGCGATG	CACTGGACCT	GGTACCTCGC	1020
35	CACCATGTTC	CTGTTCATCA	AGGATCCCGT	CAACATGCTG	GTGTACTTTT	TGGTGTCGCA	1080
	GGCGGTGTGC	GGAAACTTGT	TGGCGATCGT	GTTCTCGCTC	AACCACAACG	GTATGCCTGT	1140
4 0	GATCTCGAAG	GAGGAGGCGG	TCGATATGGA	TTTCTTCACG	AAGCAGATCA	TCACGGGTCG	1200
	TGATGTCCAC	CCGGGTCTAT	TTGCCAACTG	GTTCACGGGT	GGATTGAACT	ATCAGATCGA	1260
	GCACCACTTG	TTCCCTTCGA	TGCCTCGCCA	CAACTTTTCA	AAGATCCAGC	CTGCTGTCGA	1320
45	GACCCTGTGC	AAAAAGTACA	ATGTCCGATA	CCACACCACC	GGTATGATCG	AGGGAACTGC	1380
	AGAGGTCTTT	AGCCGTCTGA	ACGAGGTCTC	CAAGGCTGCC	TCCAAGATGG	GTAAGGCGCA	1440
50	GTAAAAAAA	AAACAAGGAC	GTTTTTTTC	GCCAGTGCCT	GTGCCTGTGC	CTGCTTCCCT	1500
	TGTCAAGTCG	AGCGTTTCTG	GAAAGGATCG	TTCAGTGCAG	TATCATCATT	CTCCTTTTAC	1560
	CCCCCGCTCA	TATCTCATTC	ATTTCTCTTA	TTAAACAACT	TGTTCCCCCC	TTCACCG	1617
55	(2) INFORM	ATION FOR SE	EQ ID NO:2:				

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 457 amino acids (B) TYPE: amino acid

 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

65

60

	(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	D NO	:2:						
5	Met 1 .	Ala	Ala	Ala	Pro 5	Ser	Val	Arg	Thr	Phe 10	Thr	Arg	Ala	Glu	Val 15	Leu
10	Asn	Ala	Glu	Ala 20	Leu	Asn	Glu	Gly	Lys 25	Lys	Asp	Ala	Glu	Ala 30	Pro	Phe
10	Leu	Met	Ile 35	Ile	Asp	Asn	Lys	Val 40	Tyr	Asp	Val	Arg	Glu 45	Phe	Val	Pro
15	Asp	His 50	Pro	Gly	Gly	Ser	Val 55	Ile	Leu	Thr	His	Val 60	Gly	Lys	Asp	Gly
	Thr 65	Asp	Val	Phe	Asp	Thr 70	Phe	His	Pro	Glu	Ala 75	Ala	Trp	Glu	Thr	Leu 80
20	Ala	Asn	Phe	Tyr	Val 85	Gly	Asp	Ile	Asp	Glu 90	Ser	Asp	Arg	Asp	Ile 95	Lys
25	Asn	Asp	Asp	Phe 100	Ala	Ala	Glu	Val	Arg 105	Lys	Leu	Arg	Thr	Leu 110	Phe	Gln
23	Ser	Leu	Gly 115	Tyr	Tyr	Asp	Ser	Ser 120	Lys	Ala	Tyr	Tyr	Ala 125	Phe	Lys	Val
30	Ser	Phe 130	Asn	Leu	Суз	Ile	Trp 135	Gly	Leu	Ser	Thr	Val 140	Ile	Val	Ala	Lys
	Trp 145	Gly	Gln	Thr	Ser	Thr 150	Leu	Ala	Asn	Val	Leu 155	Ser	Ala	Ala	Leu	Leu 160
35	Gly	Leu	Phe	Trp	Gln 165	Gln	Cys	Gly	Trp	Leu 170	Ala	His	Asp	Phe	Leu 175	His
40	His	Gln	Val	Phe 180	Gln	Asp	Arg	Phe	Trp 185	Gly	Asp	Leu	Phe	Gly 190	Ala	Phe
	Leu	Gly	Gly 195	Val	Cys	Gln	Gly	Phe 200	Ser	Ser	Ser	Trp	Trp 205	Lys	Asp	Lys
45	His	Asn 210	Thr	His	His	Ala	Ala 215	Pro	Asn	Val	His	Gly 220	Glu	Asp	Pro	Asp
	Ile 225	Asp	Thr	His	Pro	Leu 230	Leu	Thr	Trp	Ser	Glu 235	His	Ala	Leu	Glu	Met 240
50	Phe	Ser	Asp	Val	Pro 245	Asp	Glu	Glu	Leu	Thr 250	Arg	Met	Trp	Ser	Arg 255	Phe
55	Met	Val	Leu	Asn 260	Gln	Thr	Trp	Phe	Tyr 265	Phe	Pro	Ile	Leu	Ser 270	Phe	Ala
	Arg	Leu	Ser 275	Trp	Cys	Leu	Gln	Ser 280	Ile	Leu	Phe	Val	Leu 285	Pro	Asn	Gly
60	Gln	Ala 290	His	Lys	Pro	Ser	Gly 295	Ala	Arg	Val	Pro	11e 300	Ser	Leu	Val	Glu
	Gln 305	Leu	Ser	Leu	Ala	Met 310	His	Trp	Thr	Trp	Tyr 315	Leu	Ala	Thr	Met	Phe 320
65	Leu	Phe	Ile	Lys	Asp	Pro	Val	Asn -14		Leu	Val	Tyr	Phe	Leu	Val	Ser

SUBSTITUTE SHEET

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5	Gln	Ala	Val	Cys 340	Gly	Asn	Leu	Leu	Ala 345	Ile	Val	Phe	Ser	Leu 350	Asn	His	
J	Asn	Gly	Met 355	Pro	Val	Ile	Ser	Lys 360	Glu	Glu	Ala	Val	Asp 365	Met	Asp	Phe	
10	Phe	Thr 370	Lys	Gln	Ile	Ile	Thr 375	Gly	Arg	Asp	Val	His 380	Pro	Gly	Leu	Phe	
	Ala 385	Asn	Trp	Phe	Thr	Gly 390	Gly	Leu	Asn	Tyr	Gln 395	Ile	Glu	His	His	Leu 400	
15	Phe	Pro	Ser	Met	Pro 405	Arg	His	Asn	Phe	Ser 410	Lys	Ile	Gln	Pro	Ala 415	Val	
20	Glu	Thr	Leu	Cys 420	Lys	Lys	Tyr	Asn	Val 425	Arg	Tyr	His	Thr	Thr 430	Gly	Met	
	Ile	Glu	Gly 435	Thr	Ala	Glu	Val	Phe 440	Ser	Arg	Leu	Asn	Glu 445	Val	Ser	Lys	
25	Ala	Ala 450	Ser	Lys	Met	Gly	Lys 455	Ala	Gln								
	(2) INFOR	TAM	ON E	FOR S	EQ 1	D NC	3:										
30	(i)	(A) (B) (C)	LEN TYE STR	CHA IGTH: PE: D RANDE	148 ucle	88 ba eic a SS: s	se p cid singl	airs	ı								
35	(ii)	MOLE	CULE	TYF	E: D	NA (geno	mic)									
40	(xi)	SEQU	ENCE	DES	CRIE	TION	I: SE	Q ID	NO:	3:							
	GTCCCCTGT	C GC	TGTC	CGGCA	CAC	CCCA	TCC	TCCC	TCGC	TC C	СТСТ	GCGT	T TG	TCCT	TGGC	:	60
45	CCACCGTCT	C TC	CTCC	CACCO	TCC	GAGA	CGA	CTGC	AACT	GT A	ATCA	.GGAA	C CG	ACAA	ATAC	: 1	120
	ACGATTTCT	т тт	'TACI	CAGC	ACC	CAACT	CAA	AATC	CTCA	AC C	GCAA	CCCT	т тт	'TCAG	GATG	. 1	180
	GCACCTCCC	CA AC	ACTA	ATCGA	TGC	CGGI	TTG	ACCC	CAGCG	TC F	TATO	AGCA	с ст	cggc	CCCA	. 2	240
50	AACTCGGCC	CA AG	CCT	CCTI	CGA	AGCGC	CAAC	TACC	AGCT	cc c	CGAG	TTCA	C CA	TCAA	GGAG	; 3	300
	ATCCGAGAG	ST GO	ATC	CCTGC	CCF	ACTGC	CTTT	GAGC	GCTC	cg c	STCTC	CGTG	G TC	TCTG	CCAC	: 3	360
55	GTTGCCATC	CG AT	CTGA	ACTTG	GGC	CGTCG	CTC	TTGI	TCCT	'GG (TGCG	ACCC	A GA	TCGA	CAAG	; 4	120
55	TTTGAGAAT	rc co	TTG	ATCC	CTA	ATTTG	GCC	TGGC	CTGT	TT F	ACTGG	ATCA	T GC	AGGG	TATT	٠ 4	180
	GTCTGCACC	CG GI	GTCI	rgggī	GCI	rggci	CAC	GAGI	GTGG	TC F	ATCAG	TCCT	т ст	CGAC	стсс	: 5	540
60	AAGACCCTC	CA AC	CAACA	ACAGI	TGC	STTGG	SATC	TTGC	CACTO	GA 1	GCTC	TTGG	т сс	CCTA	CCAC	: 6	600
	TCCTGGAGA	AA TO	CTCGC	CACTO	GAA	AGCAC	CCAC	AAGG	CCAC	TG (CCAT	'ATGA	C CP	AGGA	CCAG	; 6	660
65	GTCTTTGTG	sc co	AAGA	ACCCC	сто	CCAC	GTT	GGCT	TGCC	CTC (CCAAG	GAGA	A CG	CTGC	TGCI		720

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	GCCGTTCA	.00 1	COMO	On Ch	. 0.	CCGI	GCAC	CIG	GAIG	AGG	AGGC	1000	. I	GIGA	CIII	G / C	, 0
	TTCTGGAT	GG T	GATC	CAGT	r CT	TGTT	CGGA	TGG	CCCG	CGT	ACCT	GATT.	AT G	AACG	CCTC	т 84	10
5	GGCCAAGA	CT A	CGGC	CGCT	G GA	CCTC	GCAC	TTC	CACA	CGT	ACTC	GCCC.	AT C	TTTG.	AGCC	C 90	0
	CGCAACTT	TT T	CGAC	TATTA	TA'	TCTC	GGAC	CTC	GGTG	TGT	TGGC	TGCC	CT C	GGTG	CCCT	G 96	0
10	ATCTATGC	CT C	CATG	CAGTI	GT(CGCT	CTTG	ACC	GTCA	CCA	AGTA	CTAT	AT T	GTCC	CCTA	C 102	O
	CTCTTTGT	CA A	CTTT:	rggti	GG'	CCT	GATC	ACC:	rtct:	rgc .	AGCA	CACC	GA T	CCCA	AGCT	G 108	0
	CCCCATTA	CC G	CGAG	GTGC	CTO	GGAA1	TTTC	CAG	CGTG	GAG	CTCT'	TTGC	AC C	GTTG	ACCG	C 114	0
15	TCGTTTGG	CA A	GTTC	TTGGA	CC2	TATO	GTTC	CAC	GGCA'	rtg '	TCCA	CACC	CA T	GTGG	CCCA!	r 120	0
	CACTTGTT	CT C	GCAA	ATGCC	GT.	CTAC	CCAT	GCT	GAGGA	AAG	CTAC	CTAT	CA T	CTCA	AGAA	A 126	0
20	CTGCTGGG	AG A	STACT	TATGT	GT2	ACGA	CCCA	TCC	CCGAT	rcg '	TCGT:	rgcgo	GT C	TGGA	GTC	3 132	0
	TTCCGTGA	GT G	CCGAT	TCGI	GG2	AGGAT	rcag	GGA	GACGT	rgg '	TCTT:	rttc/	AA G	AAGT/	AAAA	A 138	0
	AAAAGACA	AT GO	SACC	ACACA	CA	ACCTI	GTC	TCTA	ACAGA	ACC '	TACG:	PATC	AT G	ragco	CATAC	2 144	0
25	CACTTCATA	AA AA	AGAA	CATGA	GC1	CTAC	SAGG	CGT	STCAT	TTC (GCGC	CTCC				148	8
	(2) INFO	RMAT I	ON I	FOR S	EQ 1	ID NO):4:										
30	(i)	(A) (B) (C)	LEN TYI STF	CHA IGTH: PE: a RANDE POLOG	399 mino DNES	ami aci SS: r	ino a id not i	cids									
35	(ii)	MOLE	CULE	TYP	E: p	pepti	de										
40	(xi)	SEQU	JENCE	DES	CRI	OITS	: SE	II Q	NO:	: 4:							
	Met 1	Ala	Pro	Pro	Asn 5	Thr	Ile	Asp	Ala	Gly 10	Leu	Thr	Gln	Arg	His 15	Ile	
45				Ala 20					25					30		-	
50	Gln	Leu	Pro 35	Glu	Phe	Thr	Ile	Lys 40	Glu	Ile	Arg	Glu	Cys 45	Ile	Pro	Ala	
50	His	Cys 50	Phe	Glu	Arg	Ser	Gly 55	Leu	Arg	Gly	Leu	Cys 60	His	Val	Ala	Ile	
55	Asp 65	Leu	Thr	Trp	Ala	Ser 70	Leu	Leu	Phe	Leu	Ala 75	Ala	Thr	Gln	Ile	Asp 80	
	Lys	Phe	Glu	Asn	Pro 85	Leu	Ile	Arg	Tyr	Leu 90	Ala	Trp	Pro	Val	Tyr 95	Trp	
60	Ile	Met	Gln	Gly 100	Ile	Val	Cys	Thr	Gly 105	Val	Trp	Val	Leu	Ala 110	His	Glu	
65	Суѕ	Gly	His 115	Gln	Ser	Phe	Ser	Thr 120	Ser	Lys	Thr	Leu	Asn 125	Asn	Thr	Val	

		Gly	Trp 130	Ile	Leu	His	Ser	Met 135		Leu	Val	Pro	Tyr 140		Ser	Trp	Arg
5		Ile 145	Ser	His	Ser	Lys	His 150	His	Lys	Ala	Thr	Gly 155	His	Met	Thr	Lys	Asp 160
		Gln	Val	Phe	Val	Pro 165		Thr	Arg	Ser	Gln 170	Val	Gly	Leu	Pro	Pro 175	Lys
10		Glu	Asn	Ala	Ala 180	Ala	Ala	Val	Gln	Glu 185	Glu	Asp	Met	Ser	Val 190	His	Leu
15		Asp	Glu	Glu 195	Ala	Pro	Ile	Val	Thr 200	Leu	Phe	Trp	Met	Val 205	Ile	Gln	Phe
13		Leu	Phe 210	Gly	Trp	Pro	Ala	Tyr 215	Leu	Ile	Met	Asn	Ala 220	Ser	Gly	Gln	Asp
20		Tyr 225	Gly	Arg	Trp	Thr	Ser 230	His	Phe	His	Thr	Tyr 235	Ser	Pro	Ile	Phe	Glu 240
		Pro	Arg	Asn	Phe	Phe 245	Asp	Ile	Ile	Ile	Ser 250	Asp	Leu	Gly	Val	Leu 255	Ala
25		Ala	Leu	Gly	Ala 260	Leu	Ile	Tyr	Ala	Ser 265	Met	Gln	Leu	Ser	Leu 270	Leu	Thr
30		Val	Thr	Lys 275	Tyr	Tyr	Ile	Val	Pro 280	Tyr	Leu	Phe	Val	Asn 285	Phe	Trp	Leu
		Val	Leu 290	Ile	Thr	Phe	Leu	Gln 295	His	Thr	Asp	Pro	Lys 300	Leu	Pro	His	Tyr
35		Arg 305	Glu	Gly	Ala	Trp	Asn 310	Phe	Gln	Arg	Gly	Ala 315	Leu	Cys	Thr	Val	Asp 320
		Arg	Ser	Phe	Gly	Lys 325	Phe	Leu	Asp	His	Met 330	Phe	His	Gly	Ile	Val 335	His
40		Thr	His	Val	Ala 340	His	His	Leu	Phe	Ser 345	Gln	Met	Pro	Phe	Tyr 350	His	Ala
45		Glu	Glu	Ala 355	Thr	Tyr	His	Leu	Lys 360	Lys	Leu	Leu	Gly	Glu 365	Tyr	Tyr	Val
.5		Tyr	Asp 370	Pro	Ser	Pro	Ile	Val 375	Val	Ala	Val	Trp	Arg 380	Ser	Phe	Arg	Glu
50		Cys 385	Arg	Phe	Val	Glu	Asp 390	Gln	Gly	Asp	Val	Val 395	Phe	Phe	Lys	Lys	
	(2)	INFOR	TAMS	ON E	FOR S	SEQ :	ED NO	0:5:									
55		(i)	(A) (B) (C)	JENCE LEN TYI STI TOI	NGTH: PE: 8 RANDE	: 35! amino EDNE:	5 am: 5 ac: 5S: 1	ino a id not i	cids								
60		(ii)	MOLE	ECULE	Е ТҮІ	?E: j	pept:	ide									

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	Glu 1	Val	Arg	Lys	Leu 5	Arg	Thr	Leu	Phe	Gln 10	Ser	Leu	Gly	Tyr	Tyr 15	Asp
5	Ser	Ser	Lys	Ala 20	туг	Tyr	Ala	Phe	Lys 25	Val	Ser	Phe	Asn	Leu 30	Cys	Ile
10	Trp	Gly	Leu 35	Ser	Thr	Val	Ile	Val 40	Ala	Lys	Trp	Gly	Gln 45	Thr	Ser	Thr
	Leu	Ala 50	Asn	Val	Leu	Ser	Ala 55	Ala	Leu	Leu	Gly	Leu 60	Phe	Trp	Gln	Gln
15	Cys 65	Gly	Trp	Leu	Ala	His 70	Asp	Phe	Leu	His	His 75	Gln	Val	Phe	Gln	Asp 80
	Arg	Phe	Trp	Gly	Asp 85	Leu	Phe	Gly	Ala	Phe 90	Leu	Gly	Gly	Val	Cys 95	Gln
20	Gly	Phe	Ser	Ser 100	Ser	Trp	Trp	Lys	Asp 105	Lys	His	Asn	Thr	His 110	His	Ala
25	Ala	Pro	Asn 115	Val	His	Gly	Glu	Asp 120	Pro	Asp	Ile	Asp	Thr 125	His	Pro	Leu
	Leu	Thr 130	Trp	Ser	Glu	His	Ala 135	Leu	Glu	Met	Phe	Ser 140	Asp	Val	Pro	Asp
30	Glu 145	Glu	Leu	Thr	Arg	Met 150	Trp	Ser	Arg	Phe	Met 155	Val	Leu	Asn	Gln	Thr 160
	Trp	Phe	Tyr	Phe	Pro 165	Ile	Leu	Ser	Phe	Ala 170	Arg	Leu	Ser	Trp	Cys 175	Leu
35	Gln	Ser	Ile	Leu 180	Phe	Val	Leu	Pro	Asn 185	Gly	Gln	Ala	His	Lys 190	Pro	Ser
40	Gly	Ala	Arg 195	Val	Pro	Ile	Ser	Leu 200	Val	Glu	Gln	Leu	Ser 205	Leu	Ala	Met
	His	Trp 210	Thr	Trp	Tyr	Leu	Ala 215	Thr	Met	Phe	Leu	Phe 220	Ile	Lys	Asp	Pro
45	Val 225	Asn	Met	Leu	Val	Tyr 230	Phe	Leu	Val	Ser	Gln 235	Ala	Val	Суз	Gly	Asn 240
	Leu	Leu	Ala	Ile	Val 245	Phe	Ser	Leu	Asn	His 250	Asn	Gly	Met	Pro	Val 255	Ile
50	Ser	Lys	Glu	Glu 260	Ala	Val	Asp	Met	Asp 265	Phe	Phe	Thr	Lys	Gln 270	Ile	Ile
55	Thr	Gly	Arg 275	Asp	Val	His	Pro	Gly 280	Leu	Phe	Ala	Asn	Trp 285	Phe	Thr	Gly
	Gly	Leu 290	Asn	Tyr	Gln	Ile	Glu 295	His	His	Leu	Phe	Pro 300	Ser	Met	Pro	Arg
60	His 305	Asn	Phe	Ser	Lys	Ile 310	Gln	Pro	Ala	Val	Glu 315	Thr	Leu	Cys	Lys	Lys 320
	Tyr	Asn	Val	Arg	Tyr 325	His	Thr	Thr	Gly	Met 330	Ile	Glu	Gly	Thr	Ala 335	Glu
65	Val	Phe	Ser	Arg	Leu	Asn	Glu	Val -14		Lys	Ala	Ala	Ser	Lys	Met	Gly

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			340				345					350		
5	Lys	s Ala Glr 355												
3	(2) INFO	ORMATION	FOR SE	QIDN	0:6:									
10	(i)	(B) TY (C) ST	E CHAR. NGTH: PE: am. RANDEDI POLOGY	104 am ino ac NESS:	ino id not	acid								
15	(ii)	MOLECUL	E TYPE	: pept	ide									
20	(xi)	SEQUENC	E DESCI	RIPTIO	N: SI	EQ II	ON O	:6:						
	Val 1	. Thr Leu	Tyr Ti	nr Leu	Ala	Phe	Val	Ala 10	Ala	Asn	Ser	Leu	Gly 15	Val
25	Leu	Tyr Gly	Val Le 20	eu Ala	Cys	Pro	Ser 25	Val	Xaa	Pro	His	Gln 30	Ile	Ala
	Ala	Gly Leu 35	Leu G	ly Leu	Leu	Trp 40	Ile	Gln	Ser	Ala	Tyr 45	Ile	Gly	Xaa
30	Asp	Ser Gly 50	His Ty	yr Val	Ile 55	Met	Ser	Asn	Lys	Ser 60	Asn	Asn	Xaa	Phe
35	Ala 65	Gln Leu	Leu Se	er Gly 70	Asn	Cys	Leu	Thr	Gly 75	Ile	Ile	Ala	Trp	Trp 80
	Lys	Trp Thr	His As		His	His	Leu	Ala 90	Cys	Asn	Ser	Leu	Asp 95	Tyr
40	Gly	Pro Asn	Leu G] 100	ln His	Ile	Pro								
		RMATION												
45	(i)	(B) TY (C) ST	E CHARA NGTH: 2 PE: ami RANDEDI POLOGY:	252 am ino ac NESS: 1	ino a id not :	acids								
50	(ii)	MOLECUL	E TYPE:	: pept	ide									
55	(xi)	SEQUENC	E DESCI	RIPTIO	N: S1	II QE	ои с	:7:						
	Gly 1	Val Leu	Tyr G	ly Val	Leu	Ala	Суз	Thr 10	Ser	Val	Phe	Ala	His 15	Gln
60	Ile	e Ala Ala	Ala Le 20	eu Leu	Gly	Leu	Leu 25	Trp	Ile	Gln	Ser	Ala 30	Tyr	Ile
65	Gly	His Asp 35	Ser G	ly His	Tyr	Val 40	Ile	Met	Ser	Asn	Lys 45	Ser	Tyr	Asn
65						1.5	^							

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		Arg	Phe 50	Ala	Gln	Leu	Leu	Ser 55	Gly	Asn	Cys	Leu	Thr 60	Gly	Ile	Ser	Ile
5		Ala 65	Trp	Trp	Lys	Trp	Thr 70	His	Asn	Ala	His	His 75	Leu	Ala	Cys	Asn	Ser 80
		Leu	Asp	Tyr	Asp	Pro 85	Asp	Leu	Gln	His	Ile 90	Pro	Val	Phe	Ala	Val 95	Ser
10		Thr	Lys	Phe	Phe 100	Ser	Ser	Leu	Thr	Ser 105	Arg	Phe	Tyr	Asp	Arg 110	Lys	Leu
15		Thr	Phe	Gly 115	Pro	Val	Ala	Arg	Phe 120	Leu	Val	Ser	Tyr	Gln 125	His	Phe	Thr
		Tyr	Туг 130	Pro	Val	Asn	Суз	Phe 135	Gly	Arg	Ile	Asn	Leu 140	Phe	Ile	Gln	Thr
20		Phe 145	Leu	Leu	Leu	Phe	Ser 150	Lys	Arg	Glu	Val	Pro 155	Asp	Arg	Ala	Leu	Asn 160
		Phe	Ala	Gly	Ile	Leu 165	Val	Phe	Trp	Thr	Trp 170	Phe	Pro	Leu	Leu	Val 175	Ser
25		Cys	Leu	Pro	Asn 180	Trp	Pro	Glu	Arg	Phe 185	Phe	Phe	Val	Phe	Thr 190	Ser	Phe
30		Thr	Val	Thr 195	Ala	Leu	Gln	His	Ile 200	Gln	Phe	Thr	Leu	Asn 205	His	Phe	Ala
		Ala	Asp 210	Val	Tyr	Val	Gly	Pro 215	Pro	Thr	Gly	Ser	Asp 220	Trp	Phe	Glu	Lys
35		Gln 225	Ala	Ala	Gly	Thr	11e 230	Asp	Ile	Ser	Cys	Arg 235	Ser	Tyr	Met	Asp	Trp 240
40		Phe	Phe	Gly	Gly	Leu 245	Gln	Phe	Gln	Leu	Glu 250	His	His				
40	(2)	INFOF				-			_								
45		(1)	(A) (B) (C)	LEN TYE STF	CHA IGTH: PE: a RANDE POLOG	125 mino DNES	ami aci SS: r	.no a .d .ot r	cids								
		(ii)	MOLE	CULE	TYF	E: p	ept i	de									
50																	
		(xi)	SEQU	JENCE	E DES	CRIE	OITS	l: SE	Q II	NO:	8:						
55		Gly 1	Xaa	Xaa	Asn	Phe 5	Ala	Gly	Ile	Leu	Val 10	Phe	Trp	Thr	Trp	Phe 15	Pro
60		Leu	Leu	Val	Ser 20	Cys	Leu	Pro	Asn	Trp 25	Pro	Glu	Arg	Phe	Xaa 30	Phe	Val
-		Phe	Thr	Gly 35	Phe	Thr	Val	Thr	Ala 40	Leu	Gln	His	Ile	Gln 45	Phe	Thr	Leu
65		Asn	His 50	Phe	Ala	Ala	Asp	Val 55			Gly	Pro	Pro 60	Thr	Gly	Ser	Asp
									-15	1-							

		Trp 65	Phe	Glu	Lys	Gln	Ala 70	Ala	Gly	Thr	Ile	Asp 75	Ile	Ser	Cys	Arg	Ser 80
5		Tyr	Met	Asp	Trp	Phe 85	Phe	Cys	Gly	Leu	Gln 90	Phe	Gln	Leu	Glu	His 95	His
10		Leu	Phe	Pro	Arg 100	Leu	Pro	Arg	Суз	His 105	Leu	Arg	Lys	Val	Ser 110	Pro	Val
10		Gly	Gln	Arg 115	Gly	Phe	Gln	Arg	Lys 120	Xaa	Asn	Leu	Ser	Xaa 125			
15	(2)	INFO							~ .								
		(1)	(B)	LEI TYI	NGTH:	: 13:	l am: c ac:	ino a id	acid								
20		4221	(D)	то	POLOG	GY: 3	linea	ar	rere	vanc							
25		(ii)	MOLI	3CULI	S TYI	e: I	pept	ıde									
25		(xi)	SEOU	JENCI	E DES	SCRII	TION	I: SI	EO II	NO:	9:						
20		Pro	Ala			Val			_		Trp	Met	Ile	Thr	Phe		Val
30		1 Arg	Phe	Phe	Leu	5 Thr	Tyr	Val	Pro	Leu	10 Leu	Glv	Leu	Lvs	Ala	15 Phe	Leu
35					20					25					30		
33		GIY	Leu	35	rne	iie	vai	Arg	40	Leu	GIU	ser	Asn	45	Pne	vai	Trp
40		Val	Thr 50	Gln	Met	Asn	His	Ile 55	Pro	Met	His	Ile	Asp 60	His	Asp	Arg	Asn
		Met 65	Asp	Trp	Val	Ser	Thr 70	Gln	Leu	Gln	Ala	Thr 75	Cys	Asn	Val	His	Lys 80
45		Ser	Ala	Phe	Asn	Asp 85	Trp	Phe	Ser	Gly	His 90	Leu	Asn	Phe	Gln	Ile 95	Glu
		His	His	Leu	Phe 100	Pro	Thr	Met	Pro	Arg 105	His	Asn	Tyr	His	Xaa 110	Val	Ala
50		Pro	Leu	Val 115	Gln	Ser	Leu	Суз	Ala 120	Lys	His	Gly	Ile	Glu 125	Tyr	Gln	Ser
5.5		Lys	Pro 130	Leu													
55	(2)	INFO	RMAT	ION I	FOR S	SEQ :	ID NO	0:10	:								
60		(i)	(B)	LEI TYI	NGTH PE: 6	: 87 amino EDNE:	TERIS amin ac: SS: n lines	no ad id not :	cids	vant							
65		(ii)	MOLI	ECULI	E TY	PE: 1	pept:	ide	1.5	•							

5	(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	ои о	:10:						
_	Cys 1	s Ser	Pro	Lys	Ser 5	Ser	Pro	Thr	Arg	Asn 10	Met	Thr	Pro	Ser	Pro 15	Phe
10	Il€	Asp	Trp	Leu 20	Trp	Gly	Gly	Leu	Asn 25	Tyr	Gln	Ile	Glu	His 30	His	Leu
	Phe	Pro	Thr 35	Met	Pro	Arg	Cys	Asn 40	Leu	Asn	Arg	Суз	Met 45	Lys	Tyr	Val
15	Lys	Glu 50	Trp	Cys	Ala	Glu	Asn 55	Asn	Leu	Pro	Tyr	Leu 60	Val	Asp	Asp	Tyr
20	Phe 65	Val	Gly	Tyr	Asn	Leu 70	Asn	Leu	Gln	Gln	Leu 75	Lys	Asn	Met	Ala	Glu 80
20	Leu	Val	Gln	Ala	Lys 85	Ala	Ala									
25	(2) INFO	RMAT:	ION I	FOR S	SEQ I	ID NO	0:11:									
	(i)		JENCE LEN TYI	GTH:	143	3 am:	ino a		3							
30			STF TOF					elev	ant							
	(ii)	MOL	ECULE	E TYP	PE: p	pept:	ide									
35																
35	(xi)	SEQ	JENCE	E DES	SCRIE	PTIO	N: SE	:Q II	NO:	11:						
35 40		SEQU His									Leu	Ala	Tyr	Met	Leu 15	Val
	Arg 1		Glu	Ala	Ala 5	Arg	Gly	Gly	Thr	Arg 10					15	
	Arg 1 Cys	His	Glu Gln	Ala Trp 20	Ala 5 Thr	Arg Asp	Gly Leu	Gly Leu	Thr Trp 25	Arg 10 Ala	Ala	Ser	Phe	Туг 30	15 Ser	Arg
40 45	Arg 1 Cys Phe	His Met	Glu Gln Leu 35	Ala Trp 20 Ser	Ala 5 Thr Tyr	Arg Asp Ser	Gly Leu Pro	Gly Leu Phe 40	Thr Trp 25 Tyr	Arg 10 Ala Gly	Ala Ala	Ser Thr	Phe Gly 45	Tyr 30 Thr	15 Ser Leu	Arg Leu
40	Arg 1 Cys Phe Leu	His Met Phe	Glu Gln Leu 35 Val	Ala Trp 20 Ser Ala	Ala 5 Thr Tyr Val	Arg Asp Ser	Gly Leu Pro Val 55	Gly Leu Phe 40 Leu	Thr Trp 25 Tyr	Arg 10 Ala Gly Ser	Ala Ala His	Ser Thr Trp 60	Phe Gly 45 Phe	Tyr 30 Thr	15 Ser Leu Trp	Arg Leu Ile
40 45	Arg 1 Cys Phe Leu Thr 65	His Met Phe Phe 50	Glu Gln Leu 35 Val	Ala Trp 20 Ser Ala Asn	Ala 5 Thr Tyr Val	Arg Ser Arg Ile	Gly Leu Pro Val 55	Gly Leu Phe 40 Leu	Thr Trp 25 Tyr Glu Glu	Arg 10 Ala Gly Ser Ile	Ala Ala His Gly 75	Ser Thr Trp 60 His	Phe Gly 45 Phe Glu	Tyr 30 Thr Val Lys	15 Ser Leu Trp	Arg Leu Ile Arg
40 45 50	Arg 1 Cys Phe Leu Thr 65 Asp	His Met Phe Phe 50 Gln	Glu Gln Leu 35 Val Met	Ala Trp 20 Ser Ala Asn Ser	Ala 5 Thr Tyr Val His Ser 85	Arg Asp Ser Arg Ile 70 Gln	Gly Leu Pro Val 55 Pro	Gly Leu Phe 40 Leu Lys	Thr Trp 25 Tyr Glu Glu Ala	Arg 10 Ala Gly Ser Ile Thr 90	Ala Ala His Gly 75 Cys	Ser Thr Trp 60 His	Phe Gly 45 Phe Glu Val	Tyr 30 Thr Val Lys Glu	15 Ser Leu Trp His	Arg Leu Ile Arg 80 Ser
40 45 50	Arg 1 Cys Phe Leu Thr 65 Asp	His Met Phe Phe 50 Gln	Glu Gln Leu 35 Val Met Ala	Ala Trp 20 Ser Ala Asn Ser Asp	Ala 5 Thr Tyr Val His Ser 85 Trp	Arg Asp Ser Arg Ile 70 Gln Phe	Gly Leu Pro Val 55 Pro Leu Ser	Cly Leu Phe 40 Leu Lys Ala Gly	Thr Trp 25 Tyr Glu Glu Ala His 105	Arg 10 Ala Gly Ser Ile Thr 90 Leu	Ala Ala His Gly 75 Cys	Ser Thr Trp 60 His Asn	Phe Gly 45 Phe Glu Val	Tyr 30 Thr Val Lys Glu Ile 110	15 Ser Leu Trp His Pro 95 Glu	Arg Leu Ile Arg 80 Ser

	(2) INFORMATION FOR SEQ ID NO:12:	
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
10	(ii) MOLECULE TYPE: other nucleic acid	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	35
	(2) INFORMATION FOR SEQ ID NO:13:	
20	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	•
25	(D) TOPOLOGY: linear	
23	(ii) MOLECULE TYPE: other nucleic acid	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
	CUACUACUAC UAGGAGTCCT CTACGGTGTT TTG	33
35	(2) INFORMATION FOR SEQ ID NO:14:	
40	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
15	(ii) MOLECULE TYPE: other nucleic acid	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
50	CAUCAUCAUC AUATGATGCT CAAGCTGAAA CTG	33
	(2) INFORMATION FOR SEQ ID NO:15:	
55	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
60	(ii) MOLECULE TYPE: other nucleic acid	
65	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15: -154-	

	TACCAACTCG AGAAAATGGC TGCTGCTCCC AGTGTGAGG	39
5	(2) INFORMATION FOR SEQ ID NO:16:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: other nucleic acid	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
20	AACTGATCTA GATTACTGCG CCTTACCCAT CTTGGAGGC	39
	(2) INFORMATION FOR SEQ ID NO:17:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
30	(ii) MOLECULE TYPE: other nucleic acid	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
35	TACCAACTCG AGAAAATGGC ACCTCCCAAC ACTATCGAT	39
	(2) INFORMATION FOR SEQ ID NO:18:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs	
45	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: other nucleic acid	
	(II) MODECOLE TIPE: Other nucteic acid	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
	AACTGATCTA GATTACTTCT TGAAAAAGAC CACGTCTCC	39
	(2) INFORMATION FOR SEQ ID NO:19:	
55	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 746 nucleic acids	
60	(B) TYPE: nucleic acid(C) STRANDEDNESS: not relevant(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: nucleic acid	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

	CGTATGTCAC	TCCATTCCAA	ACTCGTTCAT	GGTATCATAA	ATATCAACAC	ATTTACGCTC	60
_	CACTCCTCTA	TGGTATTTAC	ACACTCAAAT	ATCGTACTCA	AGATTGGGAA	GCTTTTGTAA	120
5	AGGATGGTAA	AAATGGTGCA	ATTCGTGTTA	GTGTCGCCAC	AAATTTCGAT	AAGGCCGCTT	180
	ACGTCATTGG	TAAATTGTCT	TTTGTTTTCT	TCCGTTTCAT	CCTTCCACTC	CGTTATCATA	240
	GCTTTACAGA	TTTAATTTGT	TATTTCCTCA	TTGCTGAATT	CGTCTTTGGT	TGGTATCTCA	300
	CAATTAATTT	CCAAGTTAGT	CATGTCGCTG	AAGATCTCAA	ATTCTTTGCT	ACCCCTGAAA	360
	GACCAGATGA	ACCATCTCAA	ATCAATGAAG	ATTGGGCAAT	CCTTCAACTT	AAAACTACTC	420
10	AAGATTATGG	TCATGGTTCA	CTCCTTTGTA	CCTTTTTTAG	TGGTTCTTTA	AATCATCAAG	480
	TTGTTCATCA	TTTATTCCCA	TCAATTGCTC	AAGATTTCTA	CCCACAACTT	GTACCAATTG	540
	TAAAAGAAGT	TTGTAAAGAA	CATAACATTA	CTTACCACAT	TAAACCAAAC	TTCACTGAAG	600
	CTATTATGTC	ACACATTAAT	TACCTTTACA	AAATGGGTAA	TGATCCAGAT	TATGTTAAAA	660
	AACCATTAGC	CTCAAAAGAT	GATTAAATGA	AATAACTTAA	AAACCAATTA	TTTACTTTTG	720
15	ACAAACAGTA	ATATTAATAA	ATACAA				746

(2) INFORMATION FOR SEQ ID NO:20:

- 20 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 227 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

30	Tyr 1	Val	Thr	Pro	Phe 5	Gln	Thr	Arg	Ser	Trp	Tyr	His	Lys	Tyr	Gln 15
	His	Ile	Tyr	Ala	Pro 20	Leu	Leu	Tyr	Gly	Ile 25	Tyr	Thr	Leu	Lys	
35	Arg	Thr	Gln	Asp	Trp 35	Glu	Ala	Phe	Val	Lys 40	Asp	Gly	Lys	Asn	
	Ala	Ile	Arg	Val	Ser 50	Val	Ala	Thr	Asn	Phe 55	Asp	Lys	Ala	Ala	Tyr 60
	Val	Ile	Gly	Lys	Leu 65	Ser	Phe	Val	Phe	Phe 70	Arg	Phe	Ile	Leu	Pro
40	Leu	Arg	Tyr	His	Ser 80	Phe	Thr	Asp	Leu	Ile 85	Cys	Tyr	Phe	Leu	Ile 90
	Ala	Glu	Phe	Val	Phe 95	Gly	Trp	Tyr	Leu	Thr 100	Ile	Asn	Phe	Gln	Val 105
45	Ser	His	Val	Ala	Glu 110	Asp	Leu	Lys	Phe	Phe 115	Ala	Thr	Pro	Glu	Arg 120
	Pro	Asp	Glu	Pro	Ser 125	Gln	Ile	Asn	Glu	Asp 130	Trp	Ala	Ile	Leu	
	Leu	Lys	Thr	Thr	Gln 140	Asp	Tyr	Gly	His	Gly 145	Ser	Leu	Leu	Суз	Thr 150
50	Phe	Phe	Ser	Gly	Ser 155	Leu	Asn	His	Gln	Val 160	Val	His	His	Leu	
	Pro	Ser	Ile	Ala	Gln 170	Asp	Phe	Tyr	Pro	Gln 175	Leu	Val	Pro	Ile	
55	Lys	Glu	Val	Суѕ	Lys 185	Glu	His	Asn	Ile	Thr 190	Tyr	His	Ile	Lys	Pro
	Asn	Phe	Thr	Glu	Ala 200	Ile	Met	Ser	His	Ile 205	Asn	Tyr	Leu	Tyr	Lys 210
	Met	Gly	Asn	Asp	Pro 215	Asp	Tyr	Val	Lys	Lys 220	Pro	Leu	Ala	Ser	
60	Asp	Asp	Xaa												

- (2) INFORMATION FOR SEQ ID NO 21:
- 65 (i) SEQUENCE CHARACTERISTICS:

-156-

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(A) LENGTH: 494 nucleic acids
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: not relevant
                    (D) TOPOLOGY: linear
 5
             (ii) MOLECULE TYPE: nucleic acid
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
10
         TTTTGGAAGG NTCCAAGTTN ACCACGGANT NGGCAAGTTN ACGGGGCGGA AANCGGTTTT
                                                                                60
         CCCCCCAAGC CTTTTGTCGA CTGGTTCTGT GGTGGCTTCC AGTACCAAGT CGACCACCAC
         TTATTCCCCA GCCTGCCCCG ACACAATCTG GCCAAGACAC ACGCACTGGT CGAATCGTTC
                                                                               180
         TGCAAGGAGT GGGGTGTCCA GTACCACGAA GCCGACCTCG TGGACGGGAC CATGGAAGTC
                                                                               240
15
         TTGCACCATT TGGGCAGCGT GGCCGGCGAA TTCGTCGTGG ATTTTGTACG CGACGGACCC
                                                                               300
         GCCATGTAAT CGTCGTTCGT GACGATGCAA GGGTTCACGC ACATCTACAC ACACTCACTC
                                                                               360
         ACACAACTAG TGTAACTCGT ATAGAATTCG GTGTCGACCT GGACCTTGTT TGACTGGTTG
                                                                               420
         GGGATAGGGT AGGTAGGCGG ACGCGTGGGT CGNCCCCGGG AATTCTGTGA CCGGTACCTG
                                                                               480
         GCCCGCGTNA AAGT
                                                                               494
20
         (2) INFORMATION FOR SEQ ID NO:22:
25
              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 87 amino acids
                   (B) TYPE: amino acid
                   (C) STRANDEDNESS: not relevant
                   (D) TOPOLOGY: linear
30
             (ii) MOLECULE TYPE: peptide
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
35
         Phe Trp Lys Xaa Pro Ser Xaa Pro Arg Xaa Xaa Gln Val Xaa Gly
                                               10
         Ala Glu Xaa Gly Phe Pro Pro Lys Pro Phe Val Asp Trp Phe Cys
                                               25
         Gly Gly Phe Gln Tyr Gln Val Asp His His Leu Phe Pro Ser Leu
40
                                               40
         Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val Glu Ser Phe
                          50
         Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu Val Asp
                          65
                                               70
45
         Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly Glu
                          65
                                              70
         Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met
                          80
                                               85
50
55
         (2) INFORMATION FOR SEQ ID NO:23:
              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 520 nucleic acids
                   (B) TYPE: amino acid
60
                   (C) STRANDEDNESS: not relevant
                   (D) TOPOLOGY: linear
             (ii) MOLECULE TYPE: nucleic acid
65
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
                                           -157-
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5	ATTTACATTT TTCTGCAGTT CGCCGTAAGT CACACCCATT TGCCCGTGAG CAACCCGGAG GATCAGCTGC ATTGGCTCGA GTACGCGCG ACCACACTGT GAACATCAGC ACCAAGTCGT GGTTTGTCAC ATGGTGGATG TCGAACCTCA ACTTTCAGAT CGAGCACCAC CTTTTCCCCA CGGCGCCCCA GTTCCGTTTC AAGGAGATCA GCCCGCGCGT CGAGGCCCTC TTCAAGCGCC	60 120 180 240 300 360
10	TCTACTCCGT CGGCCATTCC GTCGGCGACG CCAAGCGCGA CTAGCCTCTT TTCCTAGACC	420 480 520
15	(2) INFORMATION FOR SEQ ID NO:24: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 153 amino acids (B) TYPE: amino acid	
20	(C) STRANDEDNESS: not relevant (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: peptide	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
	Met Glu Phe Val Trp Ile Ala Val Arg Tyr Ala Thr Trp Phe Lys 1 15	
30	Arg His Gly Cys Ala Trp Val His Ala Gly Ala Val Val Gly His 20 25 30	
	Val Leu Val Arg Leu Trp Ser Arg Leu His Leu His Phe Ser Ala	
	Val Arg Arg Lys Ser His Pro Phe Ala Arg Glu Gln Pro Gly Gly	
35	Ser Ala Ala Leu Ala Arg Val Arg Ala Asp His Thr Val Asn Ile	
	65 70 75 Ser Thr Lys Ser Trp Phe Val Thr Trp Trp Met Ser Asn Leu Asn	
40	80 85 90 Phe Gln Ile Glu His His Leu Phe Pro Thr Ala Pro Gln Phe Arg	
40	95 100 105 Phe Lys Glu Ile Ser Pro Arg Val Glu Ala Leu Phe Lys Arg His	
	110 115 120 Gly Leu Pro Tyr Tyr Asp Met Pro Tyr Thr Ser Ala Val Ser Thr	
45	125 130 135 Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly Asp Ala	
	140 145 150 Lys Arg Asp	
50	(2) INFORMATION FOR SEQ ID NO:25:	
55	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 420 nucleic acids (B) TYPE: nucleic acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: linear 	
60	(ii) MOLECULE TYPE: nucleic acid	
60	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
65	ACGCGTCCGC CCACGCGTCC GCCGCGAGCA ACTCATCAAG GAAGGCTACT TTGACCCCTC GCTCCCGCAC ATGACGTACC GCGTGGTCGA GATTGTTGTT CTCTTCGTGC TTTCCTTTTG -158-	60 120

5	GCTGATGGGT CAGTCTTCAC CCCTCGCGCT CGCTCTCGGC ATTGTCGTCA GCGGCATCTC TCAGGGTCGC TGCGGCTGGG TAATGCATGA GATGGGCCAT GGGTCGTTCA CTGGTGTCAT TTGGCTTGAC GACCGGTTGT GCGAGTTCTT TTACCGCGTT GGTTGTGGCA TGAGCGGTCA TTACTGGAAA AACCAGCACA GCAAACACCA CGCAGCGCCA AACCGGCTCG AGCACGATGT AGATCTCAAC ACCTTGCCAT TGGTGGCCTT CAACGAGCGC GTCGTGCGCA AGGTCCGACC	180 240 300 360 420												
10	(2) INFORMATION FOR SEQ ID NO:26: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 125 amino acids (B) TYPE: amino acid													
15	(B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide													
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:													
	Arg Val Arg Pro Arg Val Arg Arg Glu Gln Leu Ile Lys Glu Gly													
25	1 5 10 15 Tyr Phe Asp Pro Ser Leu Pro His Met Thr Tyr Arg Val Val Glu													
23	20 25 30 Ile Val Val Leu Phe Val Leu Ser Phe Trp Leu Met Gly Gln Ser													
	35 40 45 Ser Pro Leu Ala Leu Ala Leu Gly Ile Val Ser Gly Ile Ser													
30	50 55 60 Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly Ser													
	65 70 75 Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Leu Cys Glu Phe Phe													
25	65 70 75 Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln													
35	80													
	95 100 105 Asp Leu Asn Thr Leu Pro Leu Val Ala Phe Asn Glu Arg Val Val													
40	110 115 120 Arg Lys Val Arg Pro													
	125													
45	(2) INFORMATION FOR SEQ ID NO:27: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1219 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single													
50	(D) TOPOLOGY: linear (ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2692004)													
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:													
	GCACGCCGAC CGGCGCCGGG AGATCCTGGC AAAGTATCCA GAGATAAAGT CCTTGATGAA	60												
60	ACCTGATCCC AATTTGATAT GGATTATAAT TATGATGGTT CTCACCCAGT TGGGTGCATT	120												
	TTACATAGTA AAAGACTTGG ACTGGAAATG GGTCATATTT GGGGCCTATG CGTTTGGCAG	180												
	TTGCATTAAC CACTCAATGA CTCTGGCTAT TCATGAGATT GCCCACAATG CTGCCTTTGG	240												
65	CAACTGCAAA GCAATGTGGA ATCGCTGGTT TGGAATGTTT GCTAATCTTC CTATTGGGAT -159-	300												

	TCCATATTCA ATTTCCTTTA AGAGGTATCA CATGGATCAT CATCGGTACC TTGGAGCTGA	360
5	TGGCGTCGAT GTAGATATTC CTACCGATTT TGAGGGCTGG TTCTTCTGTA CCGCTTTCAG	420
J	AAAGTTTATA TGGGTTATTC TTCAGCCTCT CTTTTATGCC TTTCGACCTC TGTTCATCAA	480
	CCCCAAACCA ATTACGTATC TGGAAGTTAT CAATACCGTG GCACAGGTCA CTTTTGACAT	540
10	TTTAATTTAT TACTTTTGG GAATTAAATC CTTAGTCTAC ATGTTGGCAG CATCTTTACT	600
	TGGCCTGGGT TTGCACCCAA TTTCTGGACA TTTTATAGCT GAGCATTACA TGTTCTTAAA	660
15	GGGTCATGAA ACTTACTCAT ATTATGGGCC TCTGAATTTA CTTACCTTCA ATGTGGGTTA	720
13	TCATAATGAA CATCATGATT TCCCCAACAT TCCTGGAAAA AGTCTTCCAC TGGTGAGGAA	780
	AATAGCAGCT GAATACTATG ACAACCTCCC TCACTACAAT TCCTGGATAA AAGTACTGTA	840
20	TGATTTTGTG ATGGATGATA CAATAAGTCC CTACTCAAGA ATGAAGAGGC ACCAAAAAGG	900
	AGAGATGGTG CTGGAGTAAA TATCATTAGT GCCAAAGGGA TTCTTCTCCA AAACTTTAGA	960
25	TGATAAAATG GAATTTTTGC ATTATTAAAC TTGAGACCAG TGATGCTCAG AAGCTCCCCT	1020
43	GGCACAATTT CAGAGTAAGA GCTCGGTGAT ACCAAGAAGT GAATCTGGCT TTTAAACAGT	1080
	CAGCCTGACT CTGTACTGCT CAGTTTCACT CACAGGAAAC TTGTGACTTG TGTATTATCG	1140
30	TCATTGAGGA TGTTTCACTC ATGTCTGTCA TTTTATAAGC ATATCATTTA AAAAGCTTCT	1200
	AAAAAGCTAT TTCGCCAGG	1219
35	(2) INFORMATION FOR SEQ ID NO:28:	
55	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 655 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2153526)	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
50	TTACCTTCTA CGTCCGCTTC TTCCTCACTT ATGTGCCACT ATTGGGGCTG AAAGCTTCCT	60
	GGGCCTTTTC TTCATAGTCA GGTTCCTGGA AAGCAACTGG TTTGTGTGGG TGACACAGAT	120
	GAACCATATT CCCATGCACA TTGATCATGA CCGGAACATG GACTGGGTTT CCACCCAGCT	180
55	CCAGGCCACA TGCAATGTCC ACAAGTCTGC CTTCAATGAC TGGTTCAGTG GACACCTCAA	240
	CTTCCAGATT GAGCACCATC TTTTTCCCAC GATGCCTCGA CACAATTACC ACAAAGTGGC	300
60	TCCCCTGGTG CAGTCCTTGT GTGCCAAGCA TGGCATAGAG TACCAGTCCA AGCCCCTGCT	360
00	GTCAGCCTTC GCCGACATCA TCCACTCACT AAAGGAGTCA GGGCAGCTCT GGCTAGATGC	420
	CTATCTTCAC CAATAACAAC AGCCACCCTG CCCAGTCTGG AAGAAGAGGGA GGAAGACTCT	_480
65	GGAGCCAAGG CAGAGGGGAG CTTGAGGGGAC AATGCCACTA TAGTTTAATA CTCAGAGGGG -160-	540

	GTTGGGTTTG GGGACATAAA GCCTCTGACT CAAACTCCTC CCTTTTATCT TCTAGCCACA	60
5	GTTCTAAGAC CCAAAGTGGG GGGTGGACAC AGAAGTCCCT AGGAGGGAAG GAGCT	65
	(2) INFORMATION FOR SEQ ID NO:29:	
10	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 304 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
15	(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3506132)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
20	GTCTTTTACT TTGGCAATGG CTGGATTCCT ACCCTCATCA CGGCCTTTGT CCTTGCTACC	60
20	TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA	120
	CCCAAGTGGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC	180
25	AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT	240
	CCCGATGTGA ACATGCTGCA CGTGTTTGTT CTGGGCGAAT GGCAGCCCAT CGAGTACGGC	300
30	AAGA	304
	(2) INFORMATION FOR SEQ ID NO:30:	
35	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 918 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
40	(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 3854933)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
45	CAGGGACCTA CCCCGCGCTA CTTCACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCGAG	60
43	GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT	120
	CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTTGTG	180
50	GCCTTCCACA TCAACAAGGG CCTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA	240
	CTGTCTCCAG AGCAGCCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC	300
55	CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC	360
	CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGCAG CCTGGCTCAC CCTTTGGGTC	420
	TTTGGGACGT CCTTTTTGCC CTTCCTCCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGGCC	480
60	CAGGCTGGCT GGCTGCAGCA TGACTTTGGG CACCTGTCGG TCTTCAGCAC CTCAAAGTGG	540
	AACCATCTGC TACATCATTT TGTGATTGGC CACCTGAAGG GGGCCCCCGC CAGTTGGTGG	600
65	AACCACATGC ACTTCCAGCA CCATGCCAAG CCCAACTGCT TCCGCAAAGA CCCAGACATC	660

	AACATGCATC CCTTCTTCTT TGCCTTGGGG AAGATCCTCT CTGTGGAGCT TGGGAAACAG	720
	AAGAAAAAAT ATATGCCGTA CAACCACCAG CACARATACT TCTTCCTAAT TGGGCCCCCA	780
5	GCCTTGCTGC CTCTCTACTT CCAGTGGTAT ATTTTCTATT TTGTTATCCA GCGAAAGAAG	840
	TGGGTGGACT TGGCCTGGAT CAGCAAACAG GAATACGATG AAGCCGGGCT TCCATTGTCC	900
	ACCGCAAATG CTTCTAAA	918
10		
	(2) INFORMATION FOR SEQ ID NO:31:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1686 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
20	(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 2511785)	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
25	GCCACTTAAA GGGTGCCTCT GCCAACTGGT GGAATCATCG CCACTTCCAG CACCACGCCA	60
	AGCCTAACAT CTTCCACAAG GATCCCGATG TGAACATGCT GCACGTGTTT GTTCTGGGCG	120
	AATGGCAGCC CATCGAGTAC GGCAAGAAGA AGCTGAAATA CCTGCCCTAC AATCACCAGC	180
30	ACGAATACTT CTTCCTGATT GGGCCGCCGC TGCTCATCCC CATGTATTTC CAGTACCAGA	240
	TCATCATGAC CATGATCGTC CATAAGAACT GGGTGGACCT GGCCTGGGCC GTCAGCTACT	300
35	ACATCCGGTT CTTCATCACC TACATCCCTT TCTACGGCAT CCTGGGAGCC CTCCTTTTCC	360
	TCAACTTCAT CAGGTTCCTG GAGAGCCACT GGTTTGTGTG GGTCACACAG ATGAATCACA	420
10	TCGTCATGGA GATTGACCAG GAGGCCTACC GTGACTGGTT CAGTAGCCAG CTGACAGCCA	480
40	CCTGCAACGT GGAGCAGTCC TTCTTCAACG ACTGGTTCAG TGGACACCTT AACTTCCAGA	540
	TTGAGCACCA CCTCTTCCCC ACCATGCCCC GGCACAACTT ACACAAGATC GCCCCGCTGG	600
45	TGAAGTCTCT ATGTGCCAAG CATGGCATTG AATACCAGGA GAAGCCGCTA CTGAGGGCCC	660
	TGCTGGACAT CATCAGGTCC CTGAAGAAGT CTGGGAAGCT GTGGCTGGAC GCCTACCTTC	720
50	ACAAATGAAG CCACAGCCCC CGGGACACCG TGGGGAAGGG GTGCAGGTGG GGTGATGGCC	780
50	AGAGGAATGA TGGGCTTTTG TTCTGAGGGG TGTCCGAGAG GCTGGTGTAT GCACTGCTCA	840
	CGGACCCCAT GTTGGATCTT TCTCCCTTTC TCCTCTCTT TTTCTCTTCA CATCTCCCCC	900
55	ATAGCACCCT GCCCTCATGG GACCTGCCCT CCCTCAGCCG TCAGCCATCA GCCATGGCCC	960
	TCCCAGTGCC TCCTAGCCCC TTCTTCCAAG GAGCAGAGAG GTGGCCACCG GGGGTGGCTC	1020
60	TGTCCTACCT CCACTCTCTG CCCCTAAAGA TGGGAGGAGA CCAGCGGTCC ATGGGTCTGG	1080
50	CCTGTGAGTC TCCCCTTGCA GCCTGGTCAC TAGGCATCAC CCCCGCTTTG GTTCTTCAGA	1140
	TGCTCTTGGG GTTCATAGGG GCAGGTCCTA GTCGGGCAGG GCCCCTGACC CTCCCGGCCT	1200
65	GGCTTCACTC TCCCTGACGG CTGCCATTGG TCCACCCTTT CATAGAGAGG CCTGCTTTGT -162-	1260

	TACAAAGCTC GGGTCTCCCT CCTGCAGCTC GGTTAAGTAC CCGAGGCCTC TCTTAAGATG	1320
5	TCCAGGGCCC CAGGCCCGCG GGCACAGCCA GCCCAAACCT TGGGCCCTGG AAGAGTCCTC	1380
J	CACCCCATCA CTAGAGTGCT CTGACCCTGG GCTTTCACGG GCCCCATTCC ACCGCCTCCC	1440
	CAACTTGAGC CTGTGACCTT GGGACCAAAG GGGGAGTCCC TCGTCTCTTG TGACTCAGCA	1500
10	GAGGCAGTGG CCACGTTCAG GGAGGGGCCG GCTGGCCTGG AGGCTCAGCC CACCCTCCAG	1560
	CTTTTCCTCA GGGTGTCCTG AGGTCCAAGA TTCTGGAGCA ATCTGACCCT TCTCCAAAGG	1620
15	CTCTGTTATC AGCTGGGCAG TGCCAGCCAA TCCCTGGCCA TTTGGCCCCA GGGGACGTGG	1680
13	GCCCTG	1686
20	(2) INFORMATION FOR SEQ ID NO:32: (i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 1843 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid (Contig 2535)(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
30	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
	GTCTTTTACT TTGGCAATGG CTGGATTCCT ACCCTCATCA CGGCCTTTGT CCTTGCTACC	60
35	TCTCAGGCCC AAGCTGGATG GCTGCAACAT GATTATGGCC ACCTGTCTGT CTACAGAAAA	120
	CCCAAGTGGA ACCACCTTGT CCACAAATTC GTCATTGGCC ACTTAAAGGG TGCCTCTGCC	180
	AACTGGTGGA ATCATCGCCA CTTCCAGCAC CACGCCAAGC CTAACATCTT CCACAAGGAT	240
40	CCCGATGTGA ACATGCTGCA CGTGTTTGTT CTGGGCGAAT GGCAGCCCAT CGAGTACGGC	300
	AAGAAGAAGC TGAAATACCT GCCCTACAAT CACCAGCACG AATACTTCTT CCTGATTGGG	360
45	CCGCCGCTGC TCATCCCCAT GTATTTCCAG TACCAGATCA TCATGACCAT GATCGTCCAT	420
	AAGAACTGGG TGGACCTGGC CTGGGCCGTC AGCTACTACA TCCGGTTCTT CATCACCTAC	480
	ATCCCTTTCT ACGGCATCCT GGGAGCCCTC CTTTTCCTCA ACTTCATCAG GTTCCTGGAG	540
50	AGCCACTGGT TTGTGTGGGT CACACAGATG AATCACATCG TCATGGAGAT TGACCAGGAG	600
	GCCTACCGTG ACTGGTTCAG TAGCCAGCTG ACAGCCACCT GCAACGTGGA GCAGTCCTTC	660
55	TTCAACGACT GGTTCAGTGG ACACCTTAAC TTCCAGATTG AGCACCACCT CTTCCCCACC	720
	ATGCCCCGGC ACAACTTACA CAAGATCGCC CCGCTGGTGA AGTCTCTATG TGCCAAGCAT	780
	GGCATTGAAT ACCAGGAGAA GCCGCTACTG AGGGCCCTGC TGGACATCAT CAGGTCCCTG	840
60	AAGAAGTCTG GGAAGCTGTG GCTGGACGCC TACCTTCACA AATGAAGCCA CAGCCCCCGG	900
	GACACCGTGG GGAAGGGGTG CAGGTGGGGT GATGGCCAGA GGAATGATGG GCTTTTGTTC	960
65	TGAGGGGTGT CCGAGAGGCT GGTGTATGCA CTGCTCACGG ACCCCATGTT GGATCTTTCT	1020

	CCCTTTCTCC TCTCCTTTTT CTCTTCACAT CTCCCCCATA GCACCCTGCC CTCATGGGAC	1080
	CTGCCCTCCC TCAGCCGTCA GCCATCAGCC ATGGCCCTCC CAGTGCCTCC TAGCCCCTTC	1140
5	TTCCAAGGAG CAGAGAGGTG GCCACCGGGG GTGGCTCTGT CCTACCTCCA CTCTCTGCCC	1200
	CTAAAGATGG GAGGAGACCA GCGGTCCATG GGTCTGGCCT GTGAGTCTCC CCTTGCAGCC	1260
10	TGGTCACTAG GCATCACCCC CGCTTTGGTT CTTCAGATGC TCTTGGGGTT CATAGGGGCA	1320
10	GGTCCTAGTC GGGCAGGGCC CCTGACCCTC CCGGCCTGGC TTCACTCTCC CTGACGGCTG	1380
	CCATTGGTCC ACCCTTTCAT AGAGAGGCCT GCTTTGTTAC AAAGCTCGGG TCTCCCTCCT	1440
15	GCAGCTCGGT TAAGTACCCG AGGCCTCTCT TAAGATGTCC AGGGCCCCAG GCCCGCGGGC	1500
	ACAGCCAGCC CAAACCTTGG GCCCTGGAAG AGTCCTCCAC CCCATCACTA GAGTGCTCTG	1560
20	ACCCTGGGCT TTCACGGGCC CCATTCCACC GCCTCCCCAA CTTGAGCCTG TGACCTTGGG	1620
20	ACCAAAGGGG GAGTCCCTCG TCTCTTGTGA CTCAGCAGAG GCAGTGGCCA CGTTCAGGGA	1680
	GGGGCCGGCT GGCCTGGAGG CTCAGCCCAC CCTCCAGCTT TTCCTCAGGG TGTCCTGAGG	1740
25	TCCAAGATTC TGGAGCAATC TGACCCTTCT CCAAAGGCTC TGTTATCAGC TGGGCAGTGC	1800
	CAGCCAATCC CTGGCCATTT GGCCCCAGGG GACGTGGGCC CTG	1843
35	(2) INFORMATION FOR SEQ ID NO:33: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2257 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid (Edited Contig 253538a)	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
	CAGGGACCTA CCCCGCGCTA CTTCACCTGG GACGAGGTGG CCCAGCGCTC AGGGTGCGAG	60
	GAGCGGTGGC TAGTGATCGA CCGTAAGGTG TACAACATCA GCGAGTTCAC CCGCCGGCAT	120
45	CCAGGGGGCT CCCGGGTCAT CAGCCACTAC GCCGGGCAGG ATGCCACGGA TCCCTTTGTG	180
	GCCTTCCACA TCAACAAGGG CCTTGTGAAG AAGTATATGA ACTCTCTCCT GATTGGAGAA	240
50	CTGTCTCCAG AGCAGCCCAG CTTTGAGCCC ACCAAGAATA AAGAGCTGAC AGATGAGTTC	300
	CGGGAGCTGC GGGCCACAGT GGAGCGGATG GGGCTCATGA AGGCCAACCA TGTCTTCTTC	360
	CTGCTGTACC TGCTGCACAT CTTGCTGCTG GATGGTGCAG CCTGGCTCAC CCTTTGGGTC	420
55	TTTGGGACGT CCTTTTTGCC CTTCCTCCTC TGTGCGGTGC TGCTCAGTGC AGTTCAGCAG	480
	GCCCAAGCTG GATGGCTGCA ACATGATTAT GGCCACCTGT CTGTCTACAG AAAACCCAAG	540
60	TGGAACCACC TTGTCCACAA ATTCGTCATT GGCCACTTAA AGGGTGCCTC TGCCAACTGG	600
	TGGAATCATC GCCACTTCCA GCACCACGCC AAGCCTAACA TCTTCCACAA GGATCCCGAT	660
65	TGGAATCATC GCCACTTCCA GCACCACGCC AAGCCTAACA TCTTCCACAA GGATCCCGAT GTGAACATGC TGCACGTGTT TGTTCTGGGC GAATGGCAGC CCATCGAGTA CGGCAAGAAG	660 720

60

65

	AAGCTGAAAT	ACCTGCCCTA	CAATCACCAG	CACGAATACT	TCTTCCTGAT	TGGGCCGCCG	780
	CTGCTCATCC	CCATGTATTT	CCAGTACCAG	ATCATCATGA	CCATGATCGT	CCATAAGAAC	840
5	TGGGTGGACC	TGGCCTGGGC	CGTCAGCTAC	TACATCCGGT	TCTTCATCAC	CTACATCCCT	900
	TTCTACGGCA	TCCTGGGAGC	CCTCCTTTTC	CTCAACTTCA	TCAGGTTCCT	GGAGAGCCAC	960
10	TGGTTTGTGT	GGGTCACACA	GATGAATCAC	ATCGTCATGG	AGATTGACCA	GGAGGCCTAC	1020
10	CGTGACTGGT	TCAGTAGCCA	GCTGACAGCC	ACCTGCAACG	TGGAGCAGTC	CTTCTTCAAC	1080
	GACTGGTTCA	GTGGACACCT	TAACTTCCAG	ATTGAGCACC	ACCTCTTCCC	CACCATGCCC	1140
15	CGGCACAACT	TACACAAGAT	CGCCCCGCTG	GTGAAGTCTC	TATGTGCCAA	GCATGGCATT	1200
	GAATACCAGG	AGAAGCCGCT	ACTGAGGGCC	CTGCTGGACA	TCATCAGGTC	CCTGAAGAAG	1260
20	TCTGGGAAGC	TGTGGCTGGA	CGCCTACCTT	CACAAATGAA	GCCACAGCCC	CCGGGACACC	1320
	GTGGGGAAGG	GGTGCAGGTG	GGGTGATGGC	CAGAGGAATG	ATGGGCTTTT	GTTCTGAGGG	1380
	GTGTCCGAGA	GGCTGGTGTA	TGCACTGCTC	ACGGACCCCA	TGTTGGATCT	TTCTCCCTTT	1440
25	CTCCTCTCCT	TTTTCTCTTC	ACATCTCCCC	CATAGCACCC	TGCCCTCATG	GGACCTGCCC	1500
	TCCCTCAGCC	GTCAGCCATC	AGCCATGGCC	CTCCCAGTGC	CTCCTAGCCC	CTTCTTCCAA	1560
30	GGAGCAGAGA	GGTGGCCACC	GGGGGTGGCT	CTGTCCTACC	TCCACTCTCT	GCCCCTAAAG	1620
	ATGGGAGGAG	ACCAGCGGTC	CATGGGTCTG	GCCTGTGAGT	CTCCCCTTGC	AGCCTGGTCA	1680
	CTAGGCATCA	CCCCCCCTTT	GGTTCTTCAG	ATGCTCTTGG	GGTTCATAGG	GGCAGGTCCT	1740
35	AGTCGGGCAG	GGCCCCTGAC	CCTCCCGGCC	TGGCTTCACT	CTCCCTGACG	GCTGCCATTG	1800
	GTCCACCCTT	TCATAGAGAG	GCCTGCTTTG	TTACAAAGCT	CGGGTCTCCC	TCCTGCAGCT	1860
40	CGGTTAAGTA	CCCGAGGCCT	CTCTTAAGAT	GTCCAGGGCC	CCAGGCCCGC	GGGCACAGCC	1920
. •	AGCCCAAACC	TTGGGCCCTG	GAAGAGTCCT	CCACCCCATC	ACTAGAGTGC	TCTGACCCTG	1980
	GGCTTTCACG	GGCCCCATTC	CACCGCCTCC	CCAACTTGAG	CCTGTGACCT	TGGGACCAAA	2040
45	GGGGGAGTCC	CTCGTCTCTT	GTGACTCAGC	AGAGGCAGTG	GCCACGTTCA	GGGAGGGCC	2100
	GGCTGGCCTG	GAGGCTCAGC	CCACCCTCCA	GCTTTTCCTC	AGGGTGTCCT	GAGGTCCAAG	2160
50	ATTCTGGAGC	AATCTGACCC	TTCTCCAAAG	GCTCTGTTAT	CAGCTGGGCA	GTGCCAGCCA	2220
	ATCCCTGGCC	ATTTGGCCCC	AGGGGACGTG	GGCCCTG			2257
	(0) THEODIC						

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 amino acids

 - (B) TYPE: amino acid
 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: amino acid (Translation of Contig 2692004)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

65

```
His Ala Asp Arg Arg Glu Ile Leu Ala Lys Tyr Pro Glu Ile
         Lys Ser Leu Met Lys Pro Asp Pro Asn Leu Ile Trp Ile Ile Ile
 5
                                               25
         Met Met Val Leu Thr Gln Leu Gly Ala Phe Tyr Ile Val Lys Asp
                          35
                                               40
         Leu Asp Trp Lys Trp Val Ile Phe Gly Ala Tyr Ala Phe Gly Ser
                          50
                                               55
10
         Cys Ile Asn His Ser Met Thr Leu Ala Ile His Glu Ile Ala His
                          65
                                               70
         Asn Ala Ala Phe Gly Asn Cys Lys Ala Met Trp Asn Arg Trp Phe
                          80
                                               85
         Gly Met Phe Ala Asn Leu Pro Ile Gly Ile Pro Tyr Ser Ile Ser
15
                          95
                                              100
         Phe Lys Arg Tyr His Met Asp His His Arg Tyr Leu Gly Ala Asp
                         110
                                              115
         Gly Val Asp Val Asp Ile Pro Thr Asp Phe Glu Gly Trp Phe Phe
                         125
                                              130
20
         Cys Thr Ala Phe Arg Lys Phe Ile Trp Val Ile Leu Gln Pro Leu
                         140
                                              145
                                                                   150
         Phe Tyr Ala Phe Arg Pro Leu Phe Ile Asn Pro Lys Pro Ile Thr
                         155
                                              160
         Tyr Leu Glu Val Ile Asn Thr Val Ala Gln Val Thr Phe Asp Ile
25
                         170
                                              175
         Leu-Ile Tyr Tyr Phe Leu Gly Ile Lys Ser Leu Val Tyr Met Leu
                         185
                                              190
         Ala Ala Ser Leu Leu Gly Leu Gly Leu His Pro Ile Ser Gly His
                         200
                                              205
30
         Phe Ile Ala Glu His Tyr Met Phe Leu Lys Gly His Glu Thr Tyr
                         215
                                              220
         Ser Tyr Tyr Gly Pro Leu Asn Leu Leu Thr Phe Asn Val Gly Tyr
                         230
                                              235
         His Asn Glu His His Asp Phe Pro Asn Ile Pro Gly Lys Ser Leu
35
                         245
                                              250
         Pro Leu Val Arg Lys Ile Ala Ala Glu Tyr Tyr Asp Asn Leu Pro
                         260
                                              265
         His Tyr Asn Ser Trp Ile Lys Val Leu Tyr Asp Phe Val Met Asp
                         275
                                              280
40
         Asp Thr Ile Ser Pro Tyr Ser Arg Met Lys Arg His Gln Lys Gly
                         290
                                              295
         Glu Met Val Leu Glu Xaa Ile Ser Leu Val Pro Lys Gly Phe Phe
                         305
                                              310
                                                                  315
         Ser Lys Thr Leu Asp Asp Lys Met Glu Phe Leu His Tyr Xaa Thr
45
                         320
                                              325
         Xaa Asp Gln Xaa Cys Ser Glu Ala Pro Leu Ala Gln Phe Gln Ser
                         335
         Lys Ser Ser Val Ile Pro Arg Ser Glu Ser Gly Phe Xaa Thr Val
                         350
                                              355
50
         Ser Leu Thr Leu Tyr Cys Ser Val Ser Leu Thr Gly Asn Leu Xaa
                         365
                                              370
         Leu Val Tyr Tyr Arg His Xaa Gly Cys Phe Thr His Val Cys His
                         380
                                              385
         Phe Ile Ser Ile Ser Phe Lys Lys Leu Leu Lys Ser Tyr Phe Ala
55
                         400
                                              405
                                                                  410
         Arg
```

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 218 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: amino acid (Translation of Contig 2153526)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

5															
	Tyr 1	Leu	Leu	Arg	Pro 5	Leu	Leu	Pro	His	Leu 10	Суз	Ala	Thr	Ile	Gly 15
	Ala	Glu	Ser	Phe	Leu 20	Gly	Leu	Phe	Phe	Ile 25	Val	Arg	Phe	Leu	Glu 30
10	Ser	Asn	Trp	Phe	Val 35	Trp	Val	Thr	Gln	Met 40	Asn	His	Ile	Pro	Met 45
	His	Ile	Asp	His	Asp 50	Arg	Asn	Met	Asp	Trp 55	Val	Ser	Thr	Gln	Leu 60
15	Gln	Ala	Thr	Cys	Asn 65	Val	His	Lys	Ser	Ala 70	Phe	Asn	Asp	Trp	Phe 75
	Ser	Gly	His	Leu	Asn 80	Phe	Gln	Ile	Glu	His 85	His	Leu	Phe	Pro	Thr 90
	Met	Pro	Arg	His	Asn 95	Tyr	His	Lys	Val	Ala 100	Pro	Leu	Val	Gln	Ser 105
20	Leu	Cys	Ala	Lys	His 110	Gly	Ile	Glu	туr	Gln 115	Ser	Lys	Pro	Leu	
	Ser	Ala	Phe	Ala	Asp 125	Ile	Ile	His	Ser	Leu 130	Lys	Glu	Ser	Gly	
25	Leu	Trp	Leu	Asp	Ala 140	Tyr	Leu	His	Gln	Xaa 145	Gln	Gln	Pro	Pro	
	Pro	Val	Trp	Lys	Lys 155	Arg	Arg	Lys	Thr	Leu 160	Glu	Pro	Arg	Gln	
	Gly	Ala	Xaa	Gly	Thr 170	Met	Pro	Leu	Xaa	Phe 175	Asn	Thr	Gln	Arg	
30	Leu	Gly	Leu	Gly	Thr 185	Xaa	Ser	Leu	Xaa	Leu 190	Lys	Leu	Leu	Pro	
	Ile	Phe	Xaa	Pro	Gln 200	Phe	Xaa	Asp	Pro		Trp	Gly	Val	Asp	
35	Glu	Val	Pro	Arg	Arg 215	Glu	Gly	Ala							

- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOFOLOGY: linear
 - (ii) MOLECULE TYPE: amino acid (Translation of Contig 3506132)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
- Val Phe Tyr Phe Gly Asn Gly Trp Ile Pro Thr Leu Ile Thr Ala 10 55 Phe Val Leu Ala Thr Ser Gln Ala Gln Ala Gly Trp Leu Gln His 25 Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His 40 Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala 60 50 55 Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn 65 70 Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Xaa 80 85 65

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```
(2) INFORMATION FOR SEQ ID NO: 37:
 5
              (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 306 amino acids
                    (B) TYPE: amino acid
                   (C) STRANDEDNESS: single
                   (D) TOPOLOGY: linear
10
             (ii) MOLECULE TYPE: amino acid (Translation of Contig 3854933)
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
15
         Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln
         Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val
                          20
20
         Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg
                          35
         Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val
                                               55
         Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser
25
                          65
                                               70
         Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro
                          80
                                               85
         Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala
                          95
                                              100
30
         Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe
                         110
                                             115
         Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp
                         125
                                             130
         Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu
35
                         140
                                              145
         Cys Ala Val Leu Leu Ser Ala Val Gln Ala Gln Ala Gly Trp Leu
                         155
                                             160
         Gln His Asp Phe Gly His Leu Ser Val Phe Ser Thr Ser Lys Trp
                         170
                                             175
                                                                  180
40
         Asn His Leu Leu His His Phe Val Ile Gly His Leu Lys Gly Ala
                         185
                                              190
         Pro Ala Ser Trp Trp Asn His Met His Phe Gln His His Ala Lys
                         200
                                              205
         Pro Asn Cys Phe Arg Lys Asp Pro Asp Ile Asn Met His Pro Phe
45
                         215
                                             220
         Phe Phe Ala Leu Gly Lys Ile Leu Ser Val Glu Leu Gly Lys Gln
                         230
                                             235
         Lys Lys Tyr Met Pro Tyr Asn His Gln His Xaa Tyr Phe Phe
                         245
                                              250
50
         Leu Ile Gly Pro Pro Ala Leu Leu Pro Leu Tyr Phe Gln Trp Tyr
                         260
                                                                  270
         Ile Phe Tyr Phe Val Ile Gln Arg Lys Lys Trp Val Asp Leu Ala
                         275
                                              280
         Trp Ile Ser Lys Gln Glu Tyr Asp Glu Ala Gly Leu Pro Leu Ser
55
                         290
                                              295
         Thr Ala Asn Ala Ser Lys
                         305
60
         (2) INFORMATION FOR SEQ ID NO:38:
              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 566 amino acids
                   (B) TYPE: amino acid
65
                   (C) STRANDEDNESS: single
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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: amino acid (Translation of Contig 2511785)

(xi)	SECUENCE	DESCRIPTION:	SEO	TD	NO - 38 -
\ ^ _/	SEQUENCE	DESCRIPTION:	SEU	ıυ	NO:38:

	His	Leu	Lys	Gly	Ala	Ser	Ala	Asn	Trp	Trp	Asn	His	Arg	His	
10	Gln	His	His	Ala	Lys 20	Pro	Asn	Ile	Phe		Lys	Asp	Pro	Asp	
	Asn	Met	Leu	His		Phe	Val	Leu	Gly	25 Glu 40	Trp	Gln	Pro	Ile	
15	Tyr	Gly	Lys	Lys		Leu	Lys	Tyr	Leu		Tyr	Asn	His	Gln	
	Glu	Tyr	Phe	Phe		Ile	Gly	Pro	Pro		Leu	Ile	Pro	Met	60 Tyr 75
	Phe	Gln	Tyr	Gln		Ile	Met	Thr	Met		Val	His	Lys	Asn	
20	Val	Asp	Leu	Ala		Ala	Val	Ser	Tyr		Ile	Arg	Phe	Phe	
	Thr	Tyr	Ile	Pro	Phe 110	Tyr	Gly	Ile	Leu		Ala	Leu	Leu	Phe	Leu 120
25	Asn	Phe	Ile	Arg	Phe 125	Leu	Glu	Ser	His		Phe	Val	Trp	Val	Thr 135
	Gln	Met	Asn	His	Ile 140	Val	Met	Glu	Ile		Gln	Glu	Ala	Tyr	
	Asp	Trp	Phe	Ser	Ser 155	Gln	Leu	Thr	Ala	Thr 160	Cys	Asn	Val	Glu	
30	Ser	Phe	Phe	Asn	Asp 170	Trp	Phe	Ser	Gly	His 175	Leu	Asn	Phe	Gln	Ile 180
	Glu	His	His	Leu	Phe 185	Pro	Thr	Met	Pro	Arg 190	His	Asn	Leu	His	
35	Ile	Ala	Pro	Leu	Val 200	Lys	Ser	Leu	Суз	Ala 205	Lys	His	Gly	Ile	Glu 210
					215					220			Ile		Arg 225
10					230					235			Tyr		His 240
40					245					250			Gly		255
					260					265			Xaa		270
45					275					280			Met		285
					290					295			Leu		300
50					305					310			Arg		315
50					320					325			Phe		330
					335					340			Leu		345
55					350					355			Gly		360
					365					370			Thr		375
60					380					385			Gly		390
00					400					405			Ser		410
					415					420			Ala		425
65	GIN	ser	ser	GIY	Leu 430	Pro	Pro	Ala		435	Leu	Ser	Thr	Arg	Gly 440
									-16	59-					

	Leu	Ser	Xaa	Asp	Val 445	Gln	Gly	Pro	Arg	Pro 450	Ala	Gly	Thr	Ala	Ser 455
	Pro	Asn	Leu	Gly	Pro 460	Trp	Lys	Ser	Pro	Pro 465	Pro	His	His	Xaa	Ser 470
5	Ala	Leu	Thr	Leu	Gly 475	Phe	His	Gly	Pro	His 480	Ser	Thr	Ala	Ser	Pro 485
	Thr	Xaa	Ala	Суз	Asp	Leu	Gly	Thr	Lys	Gly 495	Gly	Val	Pro	Arg	
10	Leu	Xaa	Leu	Ser	Arg 505	Gly	Ser	Gly	His		Gln	Gly	Gly	Ala	
	Trp	Pro	Gly	Gly		Ala	His	Pro	Pro		Phe	Pro	Gln	Gly	
	Leu	Arg	Ser	Lys		Leu	Glu	Gln	Ser		Pro	Ser	Pro	Lys	
15	Leu	Leu	Ser	Ala		Gln	Суз	Gln	Pro		Pro	Gly	His	Leu	
	Pro	Gly	Asp	Val		Pro	Xaa			555					300
20															
	(2)	INFO	ORMAT	TION	FOR	SEQ	ID N	10:39) :						
		(i)	SEC	QUENC	CE CE	IARAC	TERI	STIC	cs:						
25									acio	is					
	(A) LENGTH: 619 amino acids(B) TYPE: amino acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear														
		,,,,								, 					05051
30	<pre>(ii) MOLECULE TYPE: amino acid (Translation of Contig 2535) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:</pre>														
		(X1)	SEÇ	UENC	CE DE	ESCRI	PTIC	N: S	SEQ I	D NC):39:				
35	Val 1	Phe	Tyr	Phe	Gly 5	Asn	Gly	Trp	Ile	Pro 10	Thr	Leu	Ile	Thr	Ala 15
	Phe	Val	Leu	Ala	Thr 20	Ser	Gln	Ala	Gln	Ala 25	Gly	Trp	Leu	Gln	His 30
40	Asp	Tyr	Gly	His	Leu 35	Ser	Val	Tyr	Arg	Lys 40	Pro	Lys	Trp	Asn	His 45
	Leu	Val	His	Lys	Phe 50	Val	Ile	Gly	His	Leu 55	Lys	Gly	Ala	Ser	
	Asn	Trp	Trp	Asn	His 65	Arg	His	Phe	Gln	His 70	His	Ala	Lys	Pro	
45	Ile	Phe	His	Lys	Asp 80	Pro	Asp	Val	Asn		Leu	His	Val	Phe	
	Leu	Gly	Glu	Trp		Pro	Ile	Glu	Tyr		Lys	Lys	Lys	Leu	
50	Tyr	Leu	Pro	Tyr		His	Gln	His	Glu		Phe	Phe	Leu	Ile	
	Pro	Pro	Leu	Leu		Pro	Met	Tyr	Phe		Tyr	Gln	Ile	Ile	
	Thr	Met	Ile	Val		Lys	Asn	Trp	Val		Leu	Ala	Trp	Ala	Val
55	Ser	Tyr	Tyr	Ile		Phe	Phe	Ile	Thr	Tyr	Ile	Pro	Phe	Tyr	
	Ile	Leu	Gly	Ala	Leu	Leu	Phe	Leu	Asn		Ile	Arg	Phe	Leu	
					170 Val	Trp	Val	Thr	Gln	175 Met	Asn	His	Ile	Val	180 Met
60	Ser	His	Trp	Phe		•									
60					185 Glu		Tyr				Phe	Ser	Ser	Gln	195 Leu
60	Glu	Ile	Asp	Gln	185 Glu 200 Asn	Ala		Arg	Asp	Trp 205 Phe					195 Leu 210
60 65	Glu Thr	Ile Ala	Asp Thr	Gln Cys	185 Glu 200 Asn 215	Ala Val	Tyr	Arg Gln	Asp Ser	Trp 205 Phe 220	Phe	Asn	Asp	Trp	195 Leu 210 Phe 225

```
230
                                              235
         Met Pro Arg His Asn Leu His Lys Ile Ala Pro Leu Val Lys Ser
                          245
                                              250
         Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Glu Lys Pro Leu Leu
 5
                          260
                                              265
         Arg Ala Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys Ser Gly Lys
                         275
                                              280
         Leu Trp Leu Asp Ala Tyr Leu His Lys Xaa Ser His Ser Pro Arg
                          290
                                              295
10
         Asp Thr Val Gly Lys Gly Cys Arg Trp Gly Asp Gly Gln Arg Asn
                          305
                                              310
         Asp Gly Leu Leu Phe Xaa Gly Val Ser Glu Arg Leu Val Tyr Ala
                         320
                                              325
         Leu Leu Thr Asp Pro Met Leu Asp Leu Ser Pro Phe Leu Leu Ser
15
                         335
                                              340
         Phe Phe Ser Ser His Leu Pro His Ser Thr Leu Pro Ser Trp Asp
                         350
                                              355
                                                                   360
         Leu Pro Ser Leu Ser Arg Gln Pro Ser Ala Met Ala Leu Pro Val
                         365
                                              370
                                                                   375
20
         Pro Pro Ser Pro Phe Phe Gln Gly Ala Glu Arg Trp Pro Pro Gly
                         380
                                              385
         Val Ala Leu Ser Tyr Leu His Ser Leu Pro Leu Lys Met Gly Gly
                         400
                                              405
         Asp Gln Arg Ser Met Gly Leu Ala Cys Glu Ser Pro Leu Ala Ala
25
                         415
                                              420
         Trp Ser Leu Gly Ile Thr Pro Ala Leu Val Leu Gln Met Leu Leu
                         430
                                              435
         Gly Phe Ile Gly Ala Gly Pro Ser Arg Ala Gly Pro Leu Thr Leu
                         445
                                              450
30
         Pro Ala Trp Leu His Ser Pro Xaa Arg Leu Pro Leu Val His Pro
                         460
                                              465
                                                                   470
         Phe Ile Glu Arg Pro Ala Leu Leu Gln Ser Ser Gly Leu Pro Pro
                         475
                                              480
         Ala Ala Arg Leu Ser Thr Arg Gly Leu Ser Xaa Asp Val Gln Gly
35
                         490
                                              495
         Pro Arg Pro Ala Gly Thr Ala Ser Pro Asn Leu Gly Pro Trp Lys
                         505
                                              510
         Ser Pro Pro Pro His His Xaa Ser Ala Leu Thr Leu Gly Phe His
                         520
                                              525
                                                                  530
40
         Gly Pro His Ser Thr Ala Ser Pro Thr Xaa Ala Cys Asp Leu Gly
                         535
                                              540
         Thr Lys Gly Gly Val Pro Arg Leu Leu Xaa Leu Ser Arg Gly Ser
                         550
         Gly His Val Gln Gly Gly Ala Gly Trp Pro Gly Gly Ser Ala His
45
                         565
                                              570
         Pro Pro Ala Phe Pro Gln Gly Val Leu Arg Ser Lys Ile Leu Glu
                         580
                                              585
         Gln Ser Asp Pro Ser Pro Lys Ala Leu Leu Ser Ala Gly Gln Cys
                         595
                                              600
50
         Gln Pro Ile Pro Gly His Leu Ala Pro Gly Asp Val Gly Pro Xaa
                         610
                                              615
```

55 (2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 757 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: amino acid (Translation of Contig 253538a)
- 65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gln Gly Pro Thr Pro Arg Tyr Phe Thr Trp Asp Glu Val Ala Gln Arg Ser Gly Cys Glu Glu Arg Trp Leu Val Ile Asp Arg Lys Val Tyr Asn Ile Ser Glu Phe Thr Arg Arg His Pro Gly Gly Ser Arg Val Ile Ser His Tyr Ala Gly Gln Asp Ala Thr Asp Pro Phe Val Ala Phe His Ile Asn Lys Gly Leu Val Lys Lys Tyr Met Asn Ser Leu Leu Ile Gly Glu Leu Ser Pro Glu Gln Pro Ser Phe Glu Pro Thr Lys Asn Lys Glu Leu Thr Asp Glu Phe Arg Glu Leu Arg Ala Thr Val Glu Arg Met Gly Leu Met Lys Ala Asn His Val Phe Phe Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly Ala Ala Trp Leu Thr Leu Trp Val Phe Gly Thr Ser Phe Leu Pro Phe Leu Leu Cys Ala Val Leu Leu Ser Ala Val Gln Gln Ala Gln Ala Gly Trp Leu Gln His Asp Tyr Gly His Leu Ser Val Tyr Arg Lys Pro Lys Trp Asn His Leu Val His Lys Phe Val Ile Gly His Leu Lys Gly Ala Ser Ala Asn Trp Trp Asn His Arg His Phe Gln His His Ala Lys Pro Asn Ile Phe His Lys Asp Pro Asp Val Asn Met Leu His Val Phe Val Leu Gly Glu Trp Gln Pro Ile Glu Tyr Gly Lys Lys Lys Leu Lys Tyr Leu Pro Tyr Asn His Gln His Glu Tyr Phe Phe Leu Ile Gly Pro Pro Leu Leu Ile Pro Met Tyr Phe Gln Tyr Gln Ile Ile Met Thr Met Ile Val His Lys Asn Trp Val Asp Leu Ala Trp Ala Val Ser Tyr Tyr Ile Arg Phe Phe Ile Thr Tyr Ile Pro Phe Tyr Gly Ile Leu Gly Ala Leu Leu Phe Leu Asn Phe Ile Arg Phe Leu Glu Ser His Trp Phe Val Trp Val Thr Gln Met Asn His Ile Val Met Glu Ile Asp Gln Glu Ala Tyr Arg Asp Trp Phe Ser Ser Gln Leu Thr Ala Thr Cys Asn Val Glu Gln Ser Phe Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu His Lys Ile Ala Pro Leu Val Lys Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Glu Lys Pro Leu Leu Arg Ala Leu Leu Asp Ile Ile Arg Ser Leu Lys Lys Ser Gly Lys Leu Trp Leu Asp Ala Tyr Leu His Lys Xaa Ser His Ser Pro Arg Asp Thr Val Gly Lys Gly Cys Arg Trp Gly Asp Gly Gln Arg Asn Asp Gly Leu Leu Phe Xaa Gly Val Ser Glu Arg Leu Val Tyr Ala Leu Leu Thr Asp Pro Met Leu Asp Leu Ser Pro Phe -172-

					475					480					485
	Leu	Leu	Ser	Phe	Phe 490	Ser	Ser	His	Leu	Pro 495		Ser	Thr	Leu	Pro 500
5	Ser	Trp	Asp	Leu	Pro 505	Ser	Leu	Ser	Arg	Gln 510		Ser	Ala	Met	Ala 515
	Leu	Pro	Val	Pro	Pro 520	Ser	Pro	Phe	Phe	Gln 525	Gly	Ala	Glu	Arg	Trp 530
	Pro	Pro	Gly	Val	Ala 535	Leu	Ser	Tyr	Leu	His 540	Ser	Leu	Pro	Leu	
10	Met	Gly	Gly	Asp	Gln 550	Arg	Ser	Met	Gly	Leu 555	Ala	Cys	Glu	Ser	Pro 560
					565					570				Leu	575
15	Met	Leu	Leu	Gly	Phe 580	Ile	Gly	Ala	Gly	Pro 585	Ser	Arg	Ala	Gly	Pro 590
	Leu	Thr	Leu	Pro	Ala 595	Trp	Leu	His	Ser	Pro 600	Xaa	Arg	Leu	Pro	Leu 605
	Val	His	Pro	Phe	Ile 610	Glu	Arg	Pro	Ala	Leu 615	Leu	Gln	Ser	Ser	Gly 620
20	Leu	Pro	Pro	Ala	Ala 625	Arg	Leu	Ser	Thr	Arg 630	Gly	Leu	Ser	Xaa	Asp 635
	Val	Gln	Gly	Pro	Arg 640	Pro	Ala	Gly	Thr	Ala 645	Ser	Pro	Asn	Leu	Gly 650
25					655					660				Thr	665
					670					675				Ala	680
	Asp	Leu	Gly	Thr	Lys 685	Gly	Gly	Val	Pro	Arg 690	Leu	Leu	Xaa	Leu	Ser 695
30	Arg	Gly	Ser	Gly	His 700	Val	Gln	Gly	Gly	Ala 705	Gly	Trp	Pro	Gly	Gly 710
	Ser	Ala	His	Pro	Pro 715	Ala	Phe	Pro	Gln	Gly 720	Val	Leu	Arg	Ser	Lys 725
35	Ile	Leu	Glu	Gln	Ser 730	Asp	Pro	Ser	Pro	Lys 735	Ala	Leu	Leu	Ser	Ala 740
	Gly	Gln	Cys	Gln	Pro 745	Ile	Pro	Gly	His	Leu 750	Ala	Pro	Gly	Asp	
	Gly	Pro	Xaa												